

645							650						655		
Asp	Ala	Arg	Ala	Glu	Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Glu	Arg	Leu
			660				665						670		
Ala	Gln	Arg	Ile	Ile	Asp	Gly	Asp	Lys	Asn	Gly	Leu	Glu	Asp	Asp	Leu
			675				680						685		
Glu	Ala	Gly	Met	Lys	Glu	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Glu	Asp
			690				695						700		
Leu	Leu	Asn	Gly	Met	Lys	Thr	Val	Gly	Glu	Leu	Phe	Gly	Ser	Gly	Gln
			705				710						720		
Met	Gln	Leu	Pro	Phe	Val	Leu	Gln	Ser	Ala	Glu	Thr	Met	Lys	Thr	Ala
			725				730						735		
Val	Ala	Tyr	Leu	Glu	Pro	Phe	Met	Glu	Glu	Glu	Ala	Glu	Ala	Thr	Gly
			740				745						750		
Ser	Ala	Gln	Ala	Glu	Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys
			755				760						765		
Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser
			770				775						780		
Asn	Asn	Gly	Tyr	Asp	Val	Val	Asn	Leu	Gly	Ile	Lys	Gln	Pro	Leu	Ser
			785				790						800		
Ala	Met	Leu	Glu	Ala	Ala	Glu	Glu	His	Lys	Ala	Asp	Val	Ile	Gly	Met
			805				810						815		
Ser	Gly	Leu	Leu	Val	Lys	Ser	Thr	Val	Val						
			820				825								

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<210> 215
<211> 621
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (598)  
<223> RXN03074
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<400> 215
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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
                                         Met Thr Gln Ser Ala
                                         1                               5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
                        10                        15                        20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
                        25                        30                        35

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ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
                   40                  45                  50  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
                   55                  60                  65  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
                   70                  75                  80                  85  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                                   90                  95                  100  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                                   105                  110                  115  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
                   120                  125                  130  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
                   135                  140                  145  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
                   150                  155                  160                  165  
 cag taatttgttt tgacgacgca gta 621  
 Gln

&lt;210&gt; 216

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 216

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
           1                  5                  10                  15  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
                   20                  25                  30  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
                   35                  40                  45  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
                   50                  55                  60  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
                   65                  70                  75                  80  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
                                   85                  90                  95



Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
 145 150 155 160

Glu Ala Pro Ile Lys Gln  
 165

<210> 217  
 <211> 621  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(598)  
 <223> FRXA02906

<400> 217  
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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115  
 Met Thr Gln Ser Ala  
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg  
           120                          125                          130  
  
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547  
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                          140                          145  
  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                          155                          160                          165  
  
 cag taatttggtt tgacgacgca gta 621  
 Gln

&lt;210&gt; 218

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 218

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp  
           1                          5                          10                          15  
  
 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
                           20                          25                          30  
  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
                           35                          40                          45  
  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                          55                          60  
  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                          70                          75                          80  
  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
                           85                          90                          95  
  
 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
                           100                          105                          110  
  
 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
           115                          120                          125  
  
 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
           130                          135                          140  
  
 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr  
           145                          150                          155                          160  
  
 Glu Ala Pro Ile Lys Gln  
                           165

&lt;210&gt; 219

&lt;211&gt; 1557

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1534)

&lt;223&gt; RXN00132

&lt;400&gt; 219

aacagcttca atcaattcgg tgtccactcc aacatgtaga gtgggtgcgcg ttaaaaaagt 60

tttcctaatt ttcattttct taaaaggagc tcgccaggac atg gca cag gtt atg 115  
 Met Ala Gln Val Met  
 1 5

gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163  
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln  
 10 15 20

att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag 211  
 Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys  
 25 30 35

gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct 259  
 Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser  
 40 45 50

atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct 307  
 Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala  
 55 60 65

ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag 355  
 Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln  
 70 75 80 85

gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag 403  
 Asp Glu Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu  
 90 95 100

cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag 451  
 Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu  
 105 110 115

tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca 499  
 Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro  
 120 125 130

aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc 547  
 Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg  
 135 140 145

ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac 595  
 Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn  
 150 155 160 165

gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt 643  
 Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu  
 170 175 180

gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt 691  
 Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly  
 185 190 195

gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct 739  
 Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala  
 200 205 210

gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc 787  
 Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val  
 215 220 225

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc 835  
 Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile  
 230 235 240 245

gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg 883  
 Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val  
 250 255 260

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931  
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe  
 265 270 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979  
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn  
 280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag  
 1027  
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu  
 295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac  
 1075  
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp  
 310 315 320 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg  
 1123  
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu  
 330 335 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg  
 1171  
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu  
 345 350 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag  
 1219  
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu  
 360 365 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc  
 1267  
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg  
 375 380 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc  
 1315  
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser  
 390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac  
 1363

Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn  
 410 415 420

gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac  
 1411

Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp  
 425 430 435

gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc  
 1459

Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr  
 440 445 450

gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc  
 1507

Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly  
 455 460 465

cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag  
 1554

Pro Phe Lys Pro Glu His Tyr Arg Tyr  
 470 475

gga  
 1557

<210> 220

<211> 478

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 220

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu  
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Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu  
 20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala  
 35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile  
 50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn  
 65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser  
 85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly  
 100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp  
 115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr  
 130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro

145		150		155		160
Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met						
		165		170		175
Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala						
		180		185		190
Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg						
		195		200		205
Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn						
		210		215		220
Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr						
		225		230		240
Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met						
		245		250		255
Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly						
		260		265		270
Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu						
		275		280		285
Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val						
		290		295		300
Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala						
		305		310		320
Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys						
		325		330		335
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp						
		340		345		350
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys						
		355		360		365
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val						
		370		375		380
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro						
		385		390		400
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile						
		405		410		415
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu						
		420		425		430
Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu						
		435		440		445
Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly						
		450		455		460
Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr						
		465		470		475

<210> 221  
 <211> 128  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(105)  
 <223> FRXA00132

<400> 221  
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 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln  
 1 5 10 15  
 gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96  
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
 20 25 30  
 tac cgc tac taatgattgt cagcattgag gga 128  
 Tyr Arg Tyr  
 35

<210> 222  
 <211> 35  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 222  
 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln  
 1 5 10 15  
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His  
 20 25 30  
 Tyr Arg Tyr  
 35

<210> 223  
 <211> 1396  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1396)  
 <223> FRXA01371

<400> 223  
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 Met Ala Gln Val Met  
 1 5  
 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163  
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln

10										15										20									
att	cgt	ctt	gca	gag	tat	gag	atg	cca	ggc	ctc	atg	cag	ttg	cgc	aag														211
Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys														
			25						30					35															
gaa	ttc	gca	gac	gag	cag	cct	ttg	aag	ggc	gcc	cga	att	gct	ggc	tct														259
Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser														
		40					45						50																
atc	cac	atg	acg	gtc	cag	acc	gcc	gtg	ctt	att	gag	acc	ctc	act	gct														307
Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala														
		55				60						65																	
ttg	ggc	gct	gag	gtt	cgt	tgg	gct	tcc	tgc	aac	att	ttc	tcc	acc	cag														355
Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln														
	70				75				80					85															
gat	gag	gct	gca	gcg	gct	atc	gtt	gtc	ggc	tcc	ggc	acc	gtc	gaa	gag														403
Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	Gly	Thr	Val	Glu	Glu														
			90						95					100															
cca	gct	ggc	gtt	cca	gta	ttc	gcg	tgg	aag	ggc	gag	tca	ctg	gag	gag														451
Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu														
			105					110					115																
tac	tgg	tgg	tgc	atc	aac	cag	atc	ttc	agc	tgg	ggc	gat	gag	ctg	cca														499
Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro														
		120					125					130																	
aac	atg	atc	ctc	gac	gac	ggc	ggc	gac	gcc	acc	atg	gct	gtt	att	cgc														547
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg														
	135					140					145																		
ggc	cgc	gaa	tac	gag	cag	gct	ggc	ctg	gtt	cca	cca	gca	gag	gcc	aac														595
Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn														
	150				155					160				165															
gat	tcc	gat	gag	tac	atc	gca	ttc	ttg	ggc	atg	ctg	cgt	gag	gtt	ctt														643
Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu														
			170					175					180																
gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	gcc	gtt	aag	ggc														691
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly														
			185				190						195																
gtc	acc	gag	gaa	acc	acc	acc	ggc	gtg	cac	cgc	ctg	tac	cac	ttc	gct														739
Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala														
		200					205					210																	
gaa	gaa	ggc	gtg	ctg	cct	ttc	cca	gcg	atg	aac	gtc	aac	gac	gct	gtc														787
Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val														
	215					220					225																		
acc	aag	tcc	aag	ttt	gat	aac	aag	tac	ggc	acc	cgc	cac	tcc	ctg	atc														835
Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	Arg	His	Ser	Leu	Ile														
	230				235					240				245															
gac	ggc	atc	aac	cgc	gcc	act	gac	atg	ctc	atg	ggc	ggc	aag	aac	gtg														883
Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met	Gly	Gly	Lys	Asn	Val														
			250					255					260																



ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931  
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe  
                   265                                  270                                  275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979  
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn  
                   280                                  285                                  290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag  
 1027  
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu  
                   295                                  300                                  305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac  
 1075  
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp  
 310                                  315                                  320                                  325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg  
 1123  
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu  
                   330                                  335                                  340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg  
 1171  
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu  
                   345                                  350                                  355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag  
 1219  
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu  
                   360                                  365                                  370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc  
 1267  
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg  
                   375                                  380                                  385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc  
 1315  
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser  
 390                                  395                                  400                                  405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac  
 1363  
 Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn  
                   410                                  415                                  420

gaa gga cag tac gag aac gag gtc tac cgt ctg  
 1396  
 Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu  
                   425                                  430

&lt;210&gt; 224

&lt;211&gt; 432

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 224

Met	Ala	Gln	Val	Met	Asp	Phe	Lys	Val	Ala	Asp	Leu	Ser	Leu	Ala	Glu	1	5	10	15
Ala	Gly	Arg	His	Gln	Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	20	25	30	
Met	Gln	Leu	Arg	Lys	Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	35	40	45	
Arg	Ile	Ala	Gly	Ser	Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	50	55	60	
Glu	Thr	Leu	Thr	Ala	Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	65	70	75	80
Ile	Phe	Ser	Thr	Gln	Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	85	90	95	
Gly	Thr	Val	Glu	Glu	Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	100	105	110	
Glu	Ser	Leu	Glu	Glu	Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	115	120	125	
Gly	Asp	Glu	Leu	Pro	Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	130	135	140	
Met	Ala	Val	Ile	Arg	Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	145	150	155	160
Pro	Ala	Glu	Ala	Asn	Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	165	170	175	
Leu	Arg	Glu	Val	Leu	Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	180	185	190	
Glu	Ala	Val	Lys	Gly	Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	195	200	205	
Leu	Tyr	His	Phe	Ala	Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	210	215	220	
Val	Asn	Asp	Ala	Val	Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	225	230	235	240
Arg	His	Ser	Leu	Ile	Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met	245	250	255	
Gly	Gly	Lys	Asn	Val	Leu	Val	Cys	Gly	Tyr	Gly	Asp	Val	Gly	Lys	Gly	260	265	270	
Cys	Ala	Glu	Ala	Phe	Asp	Gly	Gln	Gly	Ala	Arg	Val	Lys	Val	Thr	Glu	275	280	285	
Ala	Asp	Pro	Ile	Asn	Ala	Leu	Gln	Ala	Leu	Met	Asp	Gly	Tyr	Ser	Val	290	295	300	
Val	Thr	Val	Asp	Glu	Ala	Ile	Glu	Asp	Ala	Asp	Ile	Val	Ile	Thr	Ala	305	310	315	320
Thr	Gly	Asn	Lys	Asp	Ile	Ile	Ser	Phe	Glu	Gln	Met	Leu	Lys	Met	Lys				

325	330	335
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp		
340	345	350
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys		
355	360	365
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val		
370	375	380
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro		
385	390	395
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile		
405	410	415
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu		
420	425	430

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(2335)  
 <223> RXN02085

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 gatccgcacg ttcggctcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115  
 Met Thr Ser Asn Phe  
 1 5  
 tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163  
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu  
 10 15 20  
 aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211  
 Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu  
 25 30 35  
 ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg 259  
 Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu  
 40 45 50  
 tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307  
 Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala  
 55 60 65  
 atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355  
 Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp  
 70 75 80 85

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403  
 Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg  
 90 95 100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451  
 Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met  
 105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499  
 Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser  
 120 125 130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547  
 Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu  
 135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595  
 Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly  
 150 155 160 165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643  
 Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro  
 170 175 180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691  
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys  
 185 190 195

tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc 739  
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr  
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787  
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr  
 215 220 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc 835  
 Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly  
 230 235 240 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883  
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly  
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
 1219  
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
 1267  
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315  
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363  
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411  
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
 1459  
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
 1507  
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
 1555  
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
 470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
 1603  
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
 1651  
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
 1699  
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
           520                                  525                                  530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
 1747  
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
           535                                  540                                  545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
 1795  
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
 550                                  555                                  560                                  565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
 1843  
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
                                   570                                  575                                  580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga  
 1891  
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg  
                                   585                                  590                                  595

gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc  
 1939  
 Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg  
           600                                  605                                  610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg  
 1987  
 Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met  
           615                                  620                                  625

tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat  
 2035  
 Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp  
 630                                  635                                  640                                  645

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc  
 2083  
 Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu  
                                   650                                  655                                  660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg  
 2131  
 Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val  
                                   665                                  670                                  675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt  
 2179  
 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly  
           680                                  685                                  690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc  
 2227  
 Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val  
           695                                  700                                  705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct  
2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala  
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc  
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile  
730 735 740

gga gca act atc taaattgggt taccgctagg aac  
2358

Gly Ala Thr Ile  
745

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<211> 745

<212> PRT

<213> *Corynebacterium glutamicum*

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Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser  
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Phe Asp Ala  
 355 360 365  
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro  
 370 375 380  
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg  
 385 390 395 400  
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr  
 405 410 415  
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala  
 420 425 430  
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met  
 435 440 445  
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu  
 450 455 460  
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr  
 465 470 475 480  
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val  
 485 490 495  
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn  
 500 505 510  
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln  
 515 520 525  
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr



530				535				540							
Ile 545	Leu	Ala	Trp	Ser	Phe 550	Val	Arg	Asp	Asp	Gln 555	Pro	Leu	Ala	Thr	Thr 560
Ala	Asp	Gln	Val	Ala 565	Leu	Ala	Leu	Arg	Asp 570	Glu	Ile	Asn	Asp	Leu 575	Ile
Glu	Ala	Gly	Ala 580	Lys	Ile	Ile	Gln	Val 585	Asp	Glu	Pro	Ala	Ile 590	Arg	Glu
Leu	Leu	Pro 595	Leu	Arg	Asp	Val	Asp 600	Lys	Pro	Ala	Tyr	Leu 605	Gln	Trp	Ser
Val 610	Asp	Ser	Phe	Arg	Leu	Ala 615	Thr	Ala	Gly	Ala 620	Pro	Asp	Asp	Val	Gln
Ile 625	His	Thr	His	Met	Cys 630	Tyr	Ser	Glu	Phe	Asn 635	Glu	Val	Ile	Ser	Ser 640
Val	Ile	Ala	Leu	Asp 645	Ala	Asp	Val	Thr	Thr 650	Ile	Glu	Ala	Ala	Arg 655	Ser
Asp	Met	Gln	Val 660	Leu	Ala	Ala	Leu	Lys 665	Ser	Ser	Gly	Phe	Glu 670	Leu	Gly
Val	Gly	Pro 675	Gly	Val	Trp	Asp	Ile 680	His	Ser	Pro	Arg	Val 685	Pro	Ser	Ala
Gln 690	Lys	Val	Asp	Gly	Leu	Leu 695	Glu	Ala	Ala	Leu	Gln 700	Ser	Val	Asp	Pro
Arg 705	Gln	Leu	Trp	Val	Asn 710	Pro	Asp	Cys	Gly	Leu 715	Lys	Thr	Arg	Gly	Trp 720
Pro	Glu	Val	Glu	Ala 725	Ser	Leu	Lys	Val	Leu 730	Val	Glu	Ser	Ala	Lys 735	Gln
Ala	Arg	Glu	Lys 740	Ile	Gly	Ala	Thr	Ile 745							

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<211> 1923
<212> DNA
<213> Corynebacterium glutamicum
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<223> FRXA02085
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Met Thr Ser Asn Phe  
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163  
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu

10										15										20										
aag	ttc	gcg	ctc	gaa	ggc	tac	tgg	aat	gga	tca	att	gaa	ggt	cgc	gaa	211														
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu															
			25					30						35																
ctt	gcg	cag	acc	gcc	cgc	caa	ttg	gtc	aac	act	gca	tcg	gat	tct	ttg	259														
Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu															
			40				45						50																	
tct	gga	ttg	gat	tcc	gtt	ccg	ttt	gca	gga	cgt	tcc	tac	tac	gac	gca	307														
Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala															
		55				60					65																			
atg	ctc	gat	acc	gcc	gct	att	ttg	ggg	gtg	ctg	ccg	gag	cgt	ttt	gat	355														
Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp															
					75					80					85															
gac	atc	gct	gat	cat	gaa	aac	gat	ggg	ctc	cca	ctg	tgg	att	gac	cgc	403														
Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg															
				90					95					100																
tac	ttt	ggc	gct	gct	cgc	ggg	act	gag	acc	ctg	cct	gca	cag	gca	atg	451														
Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met															
			105					110					115																	
acc	aag	tgg	ttt	gat	acc	aac	tac	cac	tac	ctc	gtg	ccg	gag	ttg	tct	499														
Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser															
			120				125					130																		
gcg	gat	aca	cgt	ttc	gtt	ttg	gat	gcg	tcc	gcg	ctg	att	gag	gat	ctc	547														
Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala	Leu	Ile	Glu	Asp	Leu															
			135				140					145																		
cgt	tgc	cag	cag	gtt	cgt	ggc	gtt	aat	gcc	cgc	cct	gtt	ctg	gtt	ggg	595														
Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg	Pro	Val	Leu	Val	Gly															
					155					160					165															
cca	ctg	act	ttc	ctt	tcc	ctt	gct	cgc	acc	act	gat	ggg	tcc	aat	cct	643														
Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr	Asp	Gly	Ser	Asn	Pro															
				170					175					180																
ttg	gat	cac	ctg	cct	gca	ctg	ttt	gag	gtc	tac	gag	cgc	ctc	atc	aag	691														
Leu	Asp	His	Leu	Pro	Ala	Leu	Phe	Glu	Val	Tyr	Glu	Arg	Leu	Ile	Lys															
			185					190					195																	
tct	ttc	gat	act	gag	tgg	gtt	cag	atc	gat	gag	cct	gcg	ttg	gtc	acc	739														
Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu	Pro	Ala	Leu	Val	Thr															
			200				205					210																		
gat	gtt	gct	cct	gag	gtt	ttg	gag	cag	gtc	cgc	gct	ggg	tac	acc	act	787														
Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg	Ala	Gly	Tyr	Thr	Thr															
			215			220					225																			
ttg	gct	aag	cgc	gat	ggc	gtg	ttt	gtc	aat	act	tac	ttc	ggc	tct	ggc	835														
Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly															
					235					240					245															
gat	cag	gcg	ctg	aac	act	ctt	gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc	883														
Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly	Leu	Gly	Ala	Ile	Gly															
				250					255					260																

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931  
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly  
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979  
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg  
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc  
 1027  
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg  
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac  
 1075  
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr  
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc  
 1123  
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala  
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta  
 1171  
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu  
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att  
 1219  
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile  
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc  
 1267  
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu  
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag  
 1315  
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu  
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc  
 1363  
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe  
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa  
 1411  
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu  
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat  
 1459  
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp  
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac  
 1507

Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His  
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc  
 1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu  
 470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc  
 1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser  
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg  
 1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala  
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag  
 1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys  
 520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc  
 1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser  
 535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca  
 1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala  
 550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag  
 1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys  
 570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg  
 1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr  
 585 590 595

aga cgt cga taagcctgcc tacctgcagt ggt  
 1923

Arg Arg Arg  
 600

<210> 228

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly  
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 20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr  
 35 40 45  
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg  
 50 55 60  
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu  
 65 70 75 80  
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro  
 85 90 95  
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu  
 100 105 110  
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu  
 115 120 125  
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala  
 130 135 140  
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg  
 145 150 155 160  
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr  
 165 170 175  
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr  
 180 185 190  
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu  
 195 200 205  
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg  
 210 215 220  
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr  
 225 230 235 240  
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly  
 245 250 255  
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu  
 260 265 270  
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly  
 275 280 285  
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys  
 290 295 300  
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu  
 305 310 315 320  
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val  
 325 330 335  
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu  
 340 345 350  
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala

355					360					365						
Ala	Ser	Ala	Ala	Ile	Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro	
370					375					380						
Ile	Thr	Gln	Glu	Leu	Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg	
385					390					395					400	
Val	Thr	Leu	Gln	Glu	Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	
405					410					415						
Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	
420					425					430						
Arg	Leu	Arg	Lys	Glu	Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met	
435					440					445						
Arg	Glu	Glu	Ile	Asp	Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu	
450					455					460						
Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr	
465					470					475					480	
Phe	Ser	Glu	Leu	Leu	Asp	Gly	Phe	Leu	Ser	Thr	Ala	Asn	Gly	Trp	Val	
485					490					495						
Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Arg	Pro	Pro	Val	Leu	Phe	Gly	Asn	
500					505					510						
Val	Ser	Arg	Pro	Ala	Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln	
515					520					525						
Ser	Leu	Thr	Gln	Lys	His	Val	Lys	Gly	Met	Leu	Thr	Gly	Pro	Val	Thr	
530					535					540						
Ile	Leu	Ala	Trp	Ser	Phe	Val	Arg	Asp	Asp	Gln	Pro	Leu	Ala	Thr	Thr	
545					550					555					560	
Ala	Asp	Gln	Val	Ala	Leu	Ala	Leu	Arg	Asp	Glu	Ile	Asn	Asp	Leu	Ile	
565					570					575						
Glu	Ala	Gly	Ala	Lys	Ile	Ile	Gln	Val	Asp	Glu	Pro	Ala	Ile	Arg	Glu	
580					585					590						
Leu	Leu	Pro	Ala	Thr	Arg	Arg	Arg									
595					600											

&lt;210&gt; 229

&lt;211&gt; 603

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; FRXA02086

&lt;400&gt; 229

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[illegible]

**<210> 230**

<211> 160

<212> PRT

<213> *Corynebacterium glutamicum*

**<400> 230**

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Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala  
20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu  
35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr  
 50 55 60  
 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys  
 65 70 75 80  
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His  
 85 90 95  
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala  
 100 105 110  
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys  
 115 120 125  
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val  
 130 135 140  
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile  
 145 150 155 160

<210> 231  
 <211> 1326  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1303)  
 <223> RXN02648

<400> 231  
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 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
 Met Ser Gln Asn Arg  
 1 5  
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
 10 15 20  
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe  
 25 30 35  
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
 40 45 50  
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg



70	75	80	85	
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa				403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu				
	90	95	100	
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat				451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp				
	105	110	115	
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct				499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser				
	120	125	130	
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga				547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly				
	135	140	145	
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg				595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu				
	150	155	160	165
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca				643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala				
	170	175	180	
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac				691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp				
	185	190	195	
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa				739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu				
	200	205	210	
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg				787
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro				
	215	220	225	
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag				835
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys				
	230	235	240	245
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca				883
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala				
	250	255	260	
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc				931
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly				
	265	270	275	
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att				979
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile				
	280	285	290	
ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca				
1027				
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala				
	295	300	305	
tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt				
1075				

Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu  
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  
 1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn  
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  
 1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala  
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg  
 1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu  
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta  
 1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu  
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac  
 1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
 390 395 400

aacgagggtt gct  
 1326

<210> 232

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
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Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu  
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn  
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg  
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu  
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr  
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn  
 130 135 140  
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln  
 145 150 155 160  
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr  
 165 170 175  
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr  
 180 185 190  
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp  
 195 200 205  
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val  
 210 215 220  
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro  
 225 230 235 240  
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp  
 245 250 255  
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu  
 260 265 270  
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro  
 275 280 285  
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe  
 290 295 300  
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp  
 305 310 315 320  
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val  
 325 330 335  
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg  
 340 345 350  
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser  
 355 360 365  
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala  
 370 375 380  
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu  
 385 390 395 400  
 Phe

&lt;210&gt; 233

&lt;211&gt; 548

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (525)

&lt;223&gt; FRXA02648

&lt;400&gt; 233

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gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca      48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1              5              10              15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc      96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
              20              25              30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc     144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
              35              40              45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt     192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
  50              55              60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc     240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
  65              70              75              80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa     288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
              85              90              95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac     336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
              100              105              110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt     384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
              115              120              125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac     432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
              130              135              140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg     480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
              145              150              155              160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc         525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
              165              170              175

taagctagac aacgagggtt gct                                         548

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&lt;210&gt; 234

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 234

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Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1              5              10              15

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Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile  
                   20                  25                  30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile  
           35                  40                  45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly  
       50                  55                  60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe  
   65                  70                  75                  80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu  
                   85                  90                  95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His  
           100                  105                  110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val  
           115                  120                  125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp  
       130                  135                  140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu  
   145                  150                  155                  160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe  
                   165                  170                  175

&lt;210&gt; 235

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(784)

&lt;223&gt; FRXA02658

&lt;400&gt; 235

atgaataaaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcggttag agtcgaatga 60

gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115  
   Met Ser Gln Asn Arg  
   1                  5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163  
   Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu  
                   10                  15                  20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211  
   Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Phe  
                   25                  30                  35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259  
   Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val  
                   40                  45                  50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307  
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr  
 55 60 65  
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355  
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg  
 70 75 80 85  
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403  
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu  
 90 95 100  
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451  
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp  
 105 110 115  
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499  
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser  
 120 125 130  
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547  
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly  
 135 140 145  
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595  
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu  
 150 155 160 165  
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643  
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala  
 170 175 180  
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691  
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp  
 185 190 195  
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739  
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu  
 200 205 210  
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784  
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala  
 215 220 225

&lt;210&gt; 236

&lt;211&gt; 228

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 236

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg  
 1 5 10 15  
 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile  
 20 25 30  
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val  
 35 40 45  
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu

50	55	60	
Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn			
65	70	75	80
Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg			
	85	90	95
Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu			
	100	105	110
Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr			
	115	120	125
Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn			
	130	135	140
Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln			
	145	150	155
Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr			
	165	170	175
Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr			
	180	185	190
Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp			
	195	200	205
Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val			
	210	215	220
Gln Leu Asp Ala			
225			
<210> 237			
<211> 408			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(385)			
<223> RXC02238			
<400> 237			
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ctcttaacac tactgtccat atacttttga aaagggtgtca gtg acc aac gtg agc 115			
Val Thr Asn Val Ser 5			
aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163			
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile 20			
acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211			
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr 35			

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gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Ph
      40                      45                      50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
      55                      60                      65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
      70                      75                      80                      85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      90                      95

cac 408

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<210> 238  
 <211> 95  
 <212> PRT  
 <213> Corynebacterium glutamicum

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<400> 238
Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
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Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
      20                      25                      30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
      35                      40                      45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
      50                      55                      60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
      65                      70                      75                      80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      85                      90                      95

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<210> 239  
 <211> 1827  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1804)  
 <223> RXC00128

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<400> 239
ccaattttccg tttggtcttg cctaaagaac cgcatggaaa ttatcgtgaa gcaccgatcc 60

cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
Val Ser Lys Ile Ser
      1                      5

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acg	aaa	ctg	aag	gcc	ctc	acc	gcg	gtg	ctg	tct	gtg	acc	act	ctg	gtg	163
Thr	Lys	Leu	Lys	Ala	Leu	Thr	Ala	Val	Leu	Ser	Val	Thr	Thr	Leu	Val	
				10					15					20		
gct	ggg	tgt	tcc	acg	ctt	ccg	cag	aac	acg	gat	ccg	caa	gtg	ctg	cgc	211
Ala	Gly	Cys	Ser	Thr	Leu	Pro	Gln	Asn	Thr	Asp	Pro	Gln	Val	Leu	Arg	
			25					30					35			
tca	ttt	tcc	ggg	tcc	caa	agc	aca	caa	gag	ata	gca	ggg	ccg	acc	ccg	259
Ser	Phe	Ser	Gly	Ser	Gln	Ser	Thr	Gln	Glu	Ile	Ala	Gly	Pro	Thr	Pro	
		40					45					50				
aat	caa	gat	ccg	gat	ttg	ttg	atc	cgc	ggc	ttc	ttc	agc	gca	ggg	gcg	307
Asn	Gln	Asp	Pro	Asp	Leu	Leu	Ile	Arg	Gly	Phe	Phe	Ser	Ala	Gly	Ala	
	55					60					65					
tat	ccg	act	cag	cag	tat	gaa	gcg	gcg	aag	gcg	tat	ctg	acg	gaa	ggg	355
Tyr	Pro	Thr	Gln	Gln	Tyr	Glu	Ala	Ala	Lys	Ala	Tyr	Leu	Thr	Glu	Gly	
70					75					80					85	
acg	cgc	agc	acg	tgg	aat	ccg	gct	gcg	tcg	act	cgt	att	ttg	gat	cgc	403
Thr	Arg	Ser	Thr	Trp	Asn	Pro	Ala	Ala	Ser	Thr	Arg	Ile	Leu	Asp	Arg	
				90					95					100		
att	gat	ctg	aac	act	ctg	cca	ggg	tcg	acg	aat	gcg	gaa	cga	acg	att	451
Ile	Asp	Leu	Asn	Thr	Leu	Pro	Gly	Ser	Thr	Asn	Ala	Glu	Arg	Thr	Ile	
			105					110					115			
gcg	atc	cgt	gga	acg	cag	gtc	gga	acg	ttg	ctc	agc	ggg	ggc	gtg	tat	499
Ala	Ile	Arg	Gly	Thr	Gln	Val	Gly	Thr	Leu	Leu	Ser	Gly	Gly	Val	Tyr	
		120					125					130				
cag	ccg	gag	aat	gcg	gag	ttt	gaa	gct	gag	atc	acg	atg	cgt	cgg	gaa	547
Gln	Pro	Glu	Asn	Ala	Glu	Phe	Glu	Ala	Glu	Ile	Thr	Met	Arg	Arg	Glu	
	135					140					145					
gat	ggg	gag	tgg	cgt	atc	gat	gct	ttg	ccg	gac	ggg	att	tta	tta	gag	595
Asp	Gly	Glu	Trp	Arg	Ile	Asp	Ala	Leu	Pro	Asp	Gly	Ile	Leu	Leu	Glu	
150					155					160					165	
aga	aac	gat	ctg	cgg	aac	cat	tac	act	ccg	cac	gat	gtg	tat	ttc	ttt	643
Arg	Asn	Asp	Leu	Arg	Asn	His	Tyr	Thr	Pro	His	Asp	Val	Tyr	Phe	Phe	
			170						175					180		
gat	cct	tct	ggc	cag	gtg	ttg	gtg	ggg	gat	cgg	cgt	tgg	ttg	ttc	aat	691
Asp	Pro	Ser	Gly	Gln	Val	Leu	Val	Gly	Asp	Arg	Arg	Trp	Leu	Phe	Asn	
			185					190					195			
gag	tcg	cag	tcg	atg	tcc	acg	gtg	ctg	atg	gcc	ctt	ctg	ggt	aat	ggg	739
Glu	Ser	Gln	Ser	Met	Ser	Thr	Val	Leu	Met	Ala	Leu	Leu	Val	Asn	Gly	
		200					205					210				
cct	tcg	ccg	gca	att	tct	cct	ggg	gtg	gtc	aat	cag	ctg	tcc	acg	gat	787
Pro	Ser	Pro	Ala	Ile	Ser	Pro	Gly	Val	Val	Asn	Gln	Leu	Ser	Thr	Asp	
	215					220					225					
gcg	tcg	ttc	gtg	ggg	ttc	aat	gat	ggg	gag	tat	cag	ttc	act	ggg	ttg	835
Ala	Ser	Phe	Val	Gly	Phe	Asn	Asp	Gly	Glu	Tyr	Gln	Phe	Thr	Gly	Leu	
230					235					240					245	
gga	aat	ttg	gat	gat	gat	gcg	cgt	ttg	cgt	ttc	gcc	gcc	cag	gcc	gtg	883

Gly	Asn	Leu	Asp	Asp	Asp	Ala	Arg	Leu	Arg	Phe	Ala	Ala	Gln	Ala	Val		
				250					255					260			
tgg	acg	ttg	gcg	cat	gct	gat	gtc	gca	ggc	ccc	tac	act	ttg	gtc	gct		931
Trp	Thr	Leu	Ala	His	Ala	Asp	Val	Ala	Gly	Pro	Tyr	Thr	Leu	Val	Ala		
			265					270					275				
gac	ggc	gcg	ccg	ttg	ctg	tcg	gag	ttc	cca	acg	ctc	acc	acc	gat	gac		979
Asp	Gly	Ala	Pro	Leu	Leu	Ser	Glu	Phe	Pro	Thr	Leu	Thr	Thr	Asp	Asp		
		280					285					290					
ctc	gcc	gaa	tac	aac	cca	gag	gct	tac	acc	aac	acg	gtg	tcc	acg	ttg		
1027																	
Leu	Ala	Glu	Tyr	Asn	Pro	Glu	Ala	Tyr	Thr	Asn	Thr	Val	Ser	Thr	Leu		
	295					300					305						
ttt	gcg	ttg	cag	gat	gga	tcg	ttg	tcg	agg	gtc	agt	tcc	ggc	aat	gtg		
1075																	
Phe	Ala	Leu	Gln	Asp	Gly	Ser	Leu	Ser	Arg	Val	Ser	Ser	Gly	Asn	Val		
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agt	cca	cta	cag	ggc	att	tgg	agc	ggg	gga	gat	atc	gat	tct	gca	gcg		
1123																	
Ser	Pro	Leu	Gln	Gly	Ile	Trp	Ser	Gly	Gly	Asp	Ile	Asp	Ser	Ala	Ala		
				330					335					340			
att	tcc	tcc	tcc	gcc	aat	gtg	gtg	gca	gcg	gta	cgc	cac	gaa	aac	aac		
1171																	
Ile	Ser	Ser	Ser	Ala	Asn	Val	Val	Ala	Ala	Val	Arg	His	Glu	Asn	Asn		
			345					350					355				
gag	gca	gtg	ctt	act	gtt	ggc	tcc	atg	gaa	ggc	gtg	act	tca	gat	gcg		
1219																	
Glu	Ala	Val	Leu	Thr	Val	Gly	Ser	Met	Glu	Gly	Val	Thr	Ser	Asp	Ala		
		360					365					370					
ttg	agg	agt	gaa	acg	atc	act	cgt	ccc	acc	ttt	gaa	tac	gcg	tcg	agt		
1267																	
Leu	Arg	Ser	Glu	Thr	Ile	Thr	Arg	Pro	Thr	Phe	Glu	Tyr	Ala	Ser	Ser		
	375					380					385						
ggg	ttg	tgg	gct	gtg	gtg	gat	ggg	gag	acg	cct	gtc	cga	gtc	gca	cga		
1315																	
Gly	Leu	Trp	Ala	Val	Val	Asp	Gly	Glu	Thr	Pro	Val	Arg	Val	Ala	Arg		
390					395					400					405		
tcg	gca	aca	acc	ggg	gag	ctc	gtc	cag	acg	gag	gcg	gag	att	gtg	ctg		
1363																	
Ser	Ala	Thr	Thr	Gly	Glu	Leu	Val	Gln	Thr	Glu	Ala	Glu	Ile	Val	Leu		
				410					415					420			
cca	agg	gat	gtg	acg	ggg	ccg	atc	tct	gaa	ttc	caa	ctg	tca	cga	act		
1411																	
Pro	Arg	Asp	Val	Thr	Gly	Pro	Ile	Ser	Glu	Phe	Gln	Leu	Ser	Arg	Thr		
			425					430					435				
ggg	gtc	cgg	gcc	gcc	atg	atc	att	gaa	ggc	aag	gtg	tac	gtg	ggc	gtc		
1459																	
Gly	Val	Arg	Ala	Ala	Met	Ile	Ile	Glu	Gly	Lys	Val	Tyr	Val	Gly	Val		
		440					445						450				

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag  
1507  
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu  
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca  
1555  
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro  
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg  
1603  
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp  
490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat  
1651  
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn  
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac  
1699  
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr  
520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat  
1747  
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp  
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg  
1795  
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val  
550 555 560 565

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1827  
Val Ala Tyr

<210> 240

<211> 568

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 240

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser  
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp  
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile  
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe  
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala  
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr  
 85 90 95  
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn  
 100 105 110  
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu  
 115 120 125  
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile  
 130 135 140  
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp  
 145 150 155 160  
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His  
 165 170 175  
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg  
 180 185 190  
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala  
 195 200 205  
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn  
 210 215 220  
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr  
 225 230 235 240  
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe  
 245 250 255  
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro  
 260 265 270  
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr  
 275 280 285  
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn  
 290 295 300  
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val  
 305 310 315 320  
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp  
 325 330 335  
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val  
 340 345 350  
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly  
 355 360 365  
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe  
 370 375 380  
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro  
 385 390 395 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu  
405 410 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe  
420 425 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys  
435 440 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val  
450 455 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser  
465 470 475 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro  
485 490 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser  
500 505 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser  
515 520 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro  
530 535 540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr  
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Arg Ala Ala Pro Val Val Ala Tyr  
565

<210> 241  
<211> 1344  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1321)  
<223> RXA02240

<400> 241  
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Val Ala Gln Pro Thr  
1 5  
gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163  
Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp  
10 15 20  
aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa 211  
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu  
25 30 35  
aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga 259  
Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly

40	45	50	
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cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser 70 75 80 85			355
gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly 90 95 100			403
gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala 105 110 115			451
cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp 120 125 130			499
cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met 135 140 145			547
cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln 150 155 160 165			595
gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr 170 175 180			643
cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp 185 190 195			691
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp 200 205 210			739
ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp 215 220 225			787
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn 230 235 240 245			835
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu 250 255 260			883
acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His 265 270 275			931
ggt ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser 280 285 290			979

gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc  
1027

Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly  
295 300 305

ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca  
1075

Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala  
310 315 320 325

aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc  
1123

Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly  
330 335 340

ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg  
1171

Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu  
345 350 355

cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac  
1219

Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr  
360 365 370

gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt  
1267

Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu  
375 380 385

cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag  
1315

Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys  
390 395 400 405

ttg gcc taaaaatctg atgtagtattc ttc  
1344

Leu Ala

<210> 242

<211> 407

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 242

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr  
1 5 10 15

Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu  
20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr  
35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser  
50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile

65		70		75		80
Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val						
		85		90		95
Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp						
		100		105		110
Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg						
		115		120		125
Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu						
		130		135		140
Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser						
		145		150		155
Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg						
		165		170		175
Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg						
		180		185		190
Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu						
		195		200		205
Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp						
		210		215		220
Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile						
		225		230		235
Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met						
		245		250		255
Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly						
		260		265		270
Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser						
		275		280		285
Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn						
		290		295		300
Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr						
		305		310		315
Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp						
		325		330		335
Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu						
		340		345		350
Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu						
		355		360		365
Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg						
		370		375		380
Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu						
		385		390		395
						400



Arg Ala Ala Leu Lys Leu Ala  
405

<210> 243  
<211> 669  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(646)  
<223> RXA00780

<400> 243  
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tcacgctggt agacttgcct gcatgctctc gacaataaaaa atg atc cgt gaa gat 115  
Met Ile Arg Glu Asp  
1 5  
ctc gca aac gct cgt gaa cac gat cca gca gcc cga ggc gat tta gaa 163  
Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala Arg Gly Asp Leu Glu  
10 15 20  
aac gca gtg gtt tac tcc gga ctc cac gcc atc tgg gca cat cga gtt 211  
Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val  
25 30 35  
gcc aac agc tgg tgg aaa tcc ggt ttc cgc ggc ccc gcc cgc gta tta 259  
Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly Pro Ala Arg Val Leu  
40 45 50  
gcc caa ttc acc cga ttc ctc acc ggc att gaa att cac ccc ggt gcc 307  
Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu Ile His Pro Gly Ala  
55 60 65  
acc att ggt cgt cgc ttt ttt att gac cac gga atg gga atc gtc atc 355  
Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile  
70 75 80 85  
ggc gaa acc gct gaa atc ggc gaa ggc gtc atg ctc tac cac ggc gtc 403  
Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met Leu Tyr His Gly Val  
90 95 100  
acc ctc ggc gga cag gtt ctc acc caa acc aag cgc cac ccc acg ctc 451  
Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Leu  
105 110 115  
tgc gac aac gtg aca gtc ggc gcg ggc gca aaa atc tta ggt ccc atc 499  
Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys Ile Leu Gly Pro Ile  
120 125 130  
acc atc ggc gaa ggc tcc gca att ggc gcc aat gca gtt gtc acc aaa 547  
Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys  
135 140 145  
gac gtg ccg gca gaa cac atc gca gtc gga att cct gcg gta gca cgc 595  
Asp Val Pro Ala Glu His Ile Ala Val Gly Ile Pro Ala Val Ala Arg  
150 155 160 165

cca cgt ggc aag aca gag aag atc aag ctc gtc gat ccg gac tat tac 643  
 Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val Asp Pro Asp Tyr Tyr  
                   170                  175                  180

att taagaacagt tagcgcccta cct 669  
 Ile

<210> 244

<211> 182

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 244

Met Ile Arg Glu Asp Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala  
   1                  5                  10                  15

Arg Gly Asp Leu Glu Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile  
                   20                  25                  30

Trp Ala His Arg Val Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly  
                   35                  40                  45

Pro Ala Arg Val Leu Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu  
   50                  55                  60

Ile His Pro Gly Ala Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly  
   65                  70                  75                  80

Met Gly Ile Val Ile Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met  
                   85                  90                  95

Leu Tyr His Gly Val Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys  
                   100                  105                  110

Arg His Pro Thr Leu Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys  
                   115                  120                  125

Ile Leu Gly Pro Ile Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn  
   130                  135                  140

Ala Val Val Thr Lys Asp Val Pro Ala Glu His Ile Ala Val Gly Ile  
   145                  150                  155                  160

Pro Ala Val Ala Arg Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val  
                   165                  170                  175

Asp Pro Asp Tyr Tyr Ile  
                   180

<210> 245

<211> 1056

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1033)



ggc aag gct ggt cca cac aag atc cag ggc atc ggc gca aac ttc atc 787  
 Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile Gly Ala Asn Phe Ile  
 215 220 225

ccc gag gtc ctg gac cgc aag gtt ctc gac gac gtg ctg acc gtc tcc 835  
 Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp Val Leu Thr Val Ser  
 230 235 240 245

aac gaa gac gca atc gca ttc tcc cgc aag ctc gct acc gaa gag ggc 883  
 Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu Ala Thr Glu Glu Gly  
 250 255 260

atc ctc ggc ggt atc tcc acc ggc gca aac atc aag gca gct ctt gac 931  
 Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile Lys Ala Ala Leu Asp  
 265 270 275

ctt gca gca aag cca gag aac gct ggc aaa acc atc gtc acc gtt gtc 979  
 Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr Ile Val Thr Val Val  
 280 285 290

acc gac ttc ggc gag cgc tac gtc tcc acc gtt ctt tac gaa gac atc  
 1027  
 Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val Leu Tyr Glu Asp Ile  
 295 300 305

cgc gac taattcttag cgactgttaa cca  
 1056  
 Arg Asp  
 310

<210> 246  
 <211> 311  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 246  
 Met Gly Asn Val Tyr Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro  
 1 5 10 15  
 Leu Val Lys Leu Asn Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu  
 20 25 30  
 Val Lys Leu Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile  
 35 40 45  
 Gly Leu Ala Ile Val Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro  
 50 55 60  
 Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu  
 65 70 75 80  
 Ala Met Val Gly Ala Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro  
 85 90 95  
 Glu Thr Met Ser Asn Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala  
 100 105 110  
 Glu Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp  
 115 120 125

Lys Ala Asp Glu Ile Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg  
 130 135 140  
 Gln Phe Glu Asn Glu Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala  
 145 150 155 160  
 Lys Glu Ile Leu Glu Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala  
 165 170 175  
 Ser Phe Gly Thr Gly Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys  
 180 185 190  
 Glu Asn Asn Ala Asp Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser  
 195 200 205  
 Pro Leu Leu Thr Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile  
 210 215 220  
 Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp  
 225 230 235 240  
 Val Leu Thr Val Ser Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu  
 245 250 255  
 Ala Thr Glu Glu Gly Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile  
 260 265 270  
 Lys Ala Ala Leu Asp Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr  
 275 280 285  
 Ile Val Thr Val Val Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val  
 290 295 300  
 Leu Tyr Glu Asp Ile Arg Asp  
 305 310

<210> 247  
 <211> 623  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(600)  
 <223> RXN00402

<400> 247  
 act gac gaa aag gat gga aag cca gta ttg ccc tac ttc gtc act cca 48  
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro  
 1 5 10 15  
 gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96  
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala  
 20 25 30  
 ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc 144  
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr  
 35 40 45  
 ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt 192

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu  
 50 55 60  
 tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa 240  
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu  
 65 70 75 80  
 ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg 288  
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu  
 85 90 95  
 aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac 336  
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr  
 100 105 110  
 acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct 384  
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala  
 115 120 125  
 tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc 432  
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile  
 130 135 140  
 ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca 480  
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser  
 145 150 155 160  
 cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc 528  
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr  
 165 170 175  
 gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac 576  
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp  
 180 185 190  
 ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca 623  
 Leu Glu Gly Phe Ala Ala Ile  
 195 200  
 <210> 248  
 <211> 200  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 248  
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro  
 1 5 10 15  
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala  
 20 25 30  
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr  
 35 40 45  
 Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu  
 50 55 60  
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu  
 65 70 75 80

Phe	Leu	Asn	Asn	His 85	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu
Lys	Asp	Ser	Pro 100	Trp	Tyr	Ala	Thr	Lys 105	Glu	Lys	Leu	Gly	Leu 110	Lys	Tyr
Thr	Gly	Ser 115	Val	Leu	Thr	Phe	Glu 120	Ile	Lys	Gly	Gly	Lys 125	Asp	Glu	Ala
Trp	Ala 130	Phe	Ile	Asp	Ala	Leu 135	Lys	Leu	His	Ser	Asn 140	Leu	Ala	Asn	Ile
Gly 145	Asp	Val	Arg	Ser	Leu 150	Val	Val	His	Pro	Ala 155	Thr	Thr	Thr	His	Ser 160
Gln	Ser	Asp	Glu	Ala 165	Gly	Leu	Ala	Arg	Ala 170	Gly	Val	Thr	Gln	Ser 175	Thr
Val	Arg	Leu	Ser 180	Val	Gly	Ile	Glu	Thr 185	Ile	Asp	Asp	Ile	Ile 190	Ala	Asp
Leu	Glu	Gly 195	Gly	Phe	Ala	Ala	Ile 200								

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<210> 249
<211> 599
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(576)  
<223> FRXA00402
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<400> 249																	
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Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys		
1				5				10				15					
tac	gca	gac	ctt	ggt	gca	cca	gcc	ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc	96	
Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	Leu	Lys	Val	Arg	Val	Gly		
				20				25				30					
ctt	cta	cgc	gac	acc	ggc	tcc	acc	ctc	tcc	gca	ttc	aac	gca	tggt	gct	144	
Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala		
35				40				45									
gca	gtc	cag	ggc	atc	gac	acc	ctt	tcc	ctg	cgc	ctg	gag	cgc	cac	aac	192	
Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	Arg	Leu	Glu	Arg	His	Asn		
50				55				60									
gaa	aac	gcc	atc	aag	gtt	gca	gaa	ttc	ctc	aac	aac	cac	gag	aag	gtg	240	
Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	Phe	Leu	Asn	Asn	His	Glu	Lys	Val		
65				70				75				80					
gaa	aag	gtt	aac	ttc	gca	ggc	ctg	aag	gat	tcc	cct	tggt	tac	gca	acc	288	
Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr		
				85				90				95					
aag	gaa	aag	ctt	ggc	ctg	aag	tac	acc	ggc	tcc	gtt	ctc	acc	ttc	gag	336	

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu  
 100 105 110  
 atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384  
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys  
 115 120 125  
 cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432  
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val  
 130 135 140  
 cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480  
 His Pro Ala Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala  
 145 150 155 160  
 cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528  
 Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu  
 165 170 175  
 acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576  
 Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile  
 180 185 190  
 tagctttaaa tagactcacc cca 599

&lt;210&gt; 250

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 250

Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys  
 1 5 10 15  
 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly  
 20 25 30  
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala  
 35 40 45  
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn  
 50 55 60  
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val  
 65 70 75 80  
 Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr  
 85 90 95  
 Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu  
 100 105 110  
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys  
 115 120 125  
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val  
 130 135 140  
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala  
 145 150 155 160



Arg	Ala	Gly	Val	Thr	Gln	Ser	Thr	Val	Arg	Leu	Ser	Val	Gly	Ile	Glu
				165					170					175	
Thr	Ile	Asp	Asp	Ile	Ile	Ala	Asp	Leu	Glu	Gly	Gly	Phe	Ala	Ala	Ile
			180					185					190		

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<210> 251
<211> 613
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(613)  
<223> RXS00405
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<400> 251																
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ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac 115																
Met Pro Lys Tyr Asp 5																
aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163																
Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala 20																
ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211																
Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr 35																
caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259																
Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg 50																
ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307																
Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro 65																
acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355																
Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val 85																
cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403																
His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile 100																
ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451																
Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu 115																
tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499																
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly 130																
atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547																

Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln  
 135 140 145  
 gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595  
 Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala  
 150 155 160 165  
 aac cca cag gca gac gtc 613  
 Asn Pro Gln Ala Asp Val  
 170

<210> 252  
 <211> 171  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 252  
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr  
 1 5 10 15  
 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg  
 20 25 30  
 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu  
 35 40 45  
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser  
 50 55 60  
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser  
 65 70 75 80  
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala  
 85 90 95  
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val  
 100 105 110  
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr  
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Arg	Ala	Lys	Trp	Trp	Phe	Leu	Gly	Ala	Leu	Val	Leu	Leu	Ser	Ala	Gly	20
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Ala	Tyr	Ala	Ser	Val	Leu	Val	Pro	Gln	Val	Leu	Gly	Arg	Ile	Val	Asp	35
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Leu	Val	Ser	Asp	Gly	Ala	Gln	Met	Arg	Asp	Phe	Val	Glu	Leu	Ser	Val	50
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Ile	Leu	Ile	Ala	Val	Ala	Ile	Ala	Gly	Ala	Val	Leu	Ser	Ala	Cys	Gly	65
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Phe	Tyr	Val	Val	Ser	Arg	Ile	Ser	Glu	Lys	Ile	Ile	Ala	Asn	Leu	Arg	85
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Glu	Asp	Met	Val	Gly	Thr	Ala	Leu	Gly	Leu	Pro	Thr	His	Gln	Val	Glu	90
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Asp	Ala	Gly	Ser	Gly	Asp	Leu	Val	Ser	Arg	Ser	Thr	Asp	Asp	Val	Ser	105
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Leu	Phe	Thr	Ile	Ala	Ala	Thr	Ile	Ile	Ala	Leu	Phe	Ser	Leu	Asp	Trp	135
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Gln	Phe	Val	Leu	Ile	Pro	Val	Val	Val	Ala	Pro	Val	Tyr	Tyr	Phe	Ala	150
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Ser	Lys	His	Tyr	Leu	Ser	Lys	Ala	Pro	Asp	Arg	Tyr	Ala	Ala	Glu	Arg	170
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Ala	Ala	Met	Ala	Glu	Arg	Ala	Arg	Lys	Val	Leu	Glu	Ala	Ile	Arg	Gly	185
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cgt	gca	act	gtg	cgg	gcg	tat	tcc	atg	gaa	gat	gcc	atg	cat	aat	cag	

Ile	Asp	Gln	Ala	Ser	Trp	Ser	Val	Val	Val	Lys	Gly	Ile	Arg	Ala	Arg		
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acc	acc	atg	ttg	att	ttg	aac	atg	tgg	atg	ctg	ttt	gcg	gaa	ttc	ctc	835	
Thr	Thr	Met	Leu	Ile	Leu	Asn	Met	Trp	Met	Leu	Phe	Ala	Glu	Phe	Leu		
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Leu	Arg	Gly	Pro	Met	Asn	Met	Phe	Met	Arg	Val	Leu	Asp	Thr	Ile	Gln		
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gac	atc	gac	atc	acg	atc	aat	tcc	ggc	gaa	act	gtc	gcg	ctc	gtg	ggc		
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Ala	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Val	Ala	Ala	Leu	Leu	Ala	Gly	Leu		
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cgg	gtg	cca	gat	caa	ggg	caa	gtg	ctt	gtc	gac	gac	ttc	ccc	gtc	tct		
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Arg	Val	Pro	Asp	Gln	Gly	Gln	Val	Leu	Val	Asp	Asp	Phe	Pro	Val	Ser		
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cac	ctc	tct	gac	cgc	gag	cgt	atc	gcc	cgc	ttg	gcc	atg	gtc	agc	cag		
1315																	
His	Leu	Ser	Asp	Arg	Glu	Arg	Ile	Ala	Arg	Leu	Ala	Met	Val	Ser	Gln		
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gag	gtt	cat	gtt	ttc	tcc	ggc	acg	ctg	cgc	cag	gat	ctc	acc	ttg	gct		
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Glu	Val	His	Val	Phe	Ser	Gly	Thr	Leu	Arg	Gln	Asp	Leu	Thr	Leu	Ala		
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1411																	

Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His Ala Leu Gly Gln Val  
 425 430 435

aat gcc ctt gac tgg ttg gag agt ctt cca gaa gga ctg gac acg gtc  
 1459

Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu Gly Leu Asp Thr Val  
 440 445 450

gtt ggt gcg cga gga atc cag cta gaa cca gtg gtg gct cag cag ttg  
 1507

Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val Val Ala Gln Gln Leu  
 455 460 465

gcg ttg gcc cgg gtg ttg ttg ctc aat ccg gcg atc gtc atc atg gat  
 1555

Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala Ile Val Ile Met Asp  
 470 475 480 485

gaa gcc acg gca gaa gca gga tcg gcg ggt gcc agc gca ctg gaa gag  
 1603

Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala Ser Ala Leu Glu Glu  
 490 495 500

gct gca gat gca gtg agc aag aac cgt tcc gca ttg gtg gtg gcg cac  
 1651

Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala Leu Val Val Ala His  
 505 510 515

cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag  
 1699

Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys  
 520 525 530

ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg  
 1747

Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly  
 535 540 545

ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga  
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Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe  
 35 40 45

Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val  
 50 55 60  
 Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile  
 65 70 75 80  
 Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro  
 85 90 95  
 Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser  
 100 105 110  
 Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro  
 115 120 125  
 Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu  
 130 135 140  
 Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro  
 145 150 155 160  
 Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg  
 165 170 175  
 Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu  
 180 185 190  
 Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp  
 195 200 205  
 Ala Met His Asn Gln Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys  
 210 215 220  
 Gly Ile Arg Ala Arg Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu  
 225 230 235 240  
 Phe Ala Glu Phe Leu Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys  
 245 250 255  
 Leu Val Ile Asp Asn Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val  
 260 265 270  
 Leu Met Ile Ile Arg Leu Arg Gly Pro Met Asn Met Phe Met Arg Val  
 275 280 285  
 Leu Asp Thr Ile Gln Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly  
 290 295 300  
 Val Val Ala Asp Pro Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala  
 305 310 315 320  
 Pro Gln Gly Lys Val Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp  
 325 330 335  
 Ser Trp Ala Val Lys Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr  
 340 345 350  
 Val Ala Leu Val Gly Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala  
 355 360 365

Leu Leu Ala Gly Leu Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp  
 370 375 380  
 Asp Phe Pro Val Ser His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu  
 385 390 395 400  
 Ala Met Val Ser Gln Glu Val His Val Phe Ser Gly Thr Leu Arg Gln  
 405 410 415  
 Asp Leu Thr Leu Ala Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His  
 420 425 430  
 Ala Leu Gly Gln Val Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu  
 435 440 445  
 Gly Leu Asp Thr Val Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val  
 450 455 460  
 Val Ala Gln Gln Leu Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala  
 465 470 475 480  
 Ile Val Ile Met Asp Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala  
 485 490 495  
 Ser Ala Leu Glu Glu Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala  
 500 505 510  
 Leu Val Val Ala His Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile  
 515 520 525  
 Leu Val Met Asp Lys Gly Glu Val Val Glu Ser Gly Thr His Gln Glu  
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 <223> RXC01191

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 Val Gly Gly Leu Val 5  
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 gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg 163  
 Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala  
 10 15 20

ctg ctt atc gtg gct ggc ggc gtt gtt tcg agc ctg ggc acg tgg tgg	211
Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp	
25 30 35	
ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg	259
Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu	
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cgc gag gat gtg ttg cgc gcg gcg gtg agt ttg gat gcg aac acg att	307
Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu Asp Ala Asn Thr Ile	
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gaa acg gcg ggg cgc ggc gac gtg att tcg cgt atc gcg gat gat tcg	355
Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg Ile Ala Asp Asp Ser	
70 75 80 85	
cgg gag gtg tcc act gcg gcg agc acc gtg gtg ccg ctg atg gtg cag	403
Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val Pro Leu Met Val Gln	
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gcg ggc ttt acc gtg gtg att tcc gcg ttt ggc atg gcg gcg gtt gat	451
Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly Met Ala Ala Val Asp	
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tgg cgc ctc ggc ctt gtc ggt ttg gtc gcg atc ccg ctg tat tgg acc	499
Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile Pro Leu Tyr Trp Thr	
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acg ttg cgc gtc tat tta ccc cgc tca ggt ccg ctt tat acg cgt gag	547
Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro Leu Tyr Thr Arg Glu	
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Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu Val Gly Ala Val Glu	
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ggc gcg gaa acc ttg cgc gct ttc cgc gca gaa gat aca gaa tta aag	643
Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu Asp Thr Glu Leu Lys	
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cgt atc gac gca gcc tcc ggc gaa gcc cgc gac att tcc att tct gtt	691
Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp Ile Ser Ile Ser Val	
185 190 195	
ttc agg ttc ctc aca tgg gca ttt tcc cgc aac aac cgc gcg gaa tgc	739
Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn Asn Arg Ala Glu Cys	
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atc acc ctc gtg ctc atc ttg ggc acc ggc ttt tac ctg gtc aac atc	787
Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe Tyr Leu Val Asn Ile	
215 220 225	
gat ctg gtc acc gtc ggc gca gtc tca acc gcc gca ctg atc ttc cac	835
Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala Ala Leu Ile Phe His	
230 235 240 245	
cga ctc ttc ggt cca atc ggc acg ctc gtg ggc atg ttc tcc gac atc	883
Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly Met Phe Ser Asp Ile	
250 255 260	
caa tcc gcc agc gca tcg ctg atc cgc atg gtg ggc gtt att aac gcg	931



Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val Gly Val Ile Asn Ala  
 265 270 275  
 gca tcg aac cag gtc agc ggc acc tcg ccg gcg tct gcc agc acc gct 979  
 Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala Ser Ala Ser Thr Ala  
 280 285 290  
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 Leu Thr Leu Phe Asp Val Ser His His Tyr His Thr Ala Pro Val Ile  
 295 300 305  
 aag aat gca tcc gtg cag ctg gaa cca ggg gaa cac atc gcc att gtg  
 1075  
 Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu His Ile Ala Ile Val  
 310 315 320 325  
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 345 350 355  
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 1219  
 Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys Ile Ala Met Val Ser  
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 Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu Asp Asn Leu Arg Ile  
 375 380 385  
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 1315  
 Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His Ala Val Leu Ala Asp  
 390 395 400 405  
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 Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln Gly Ile Asp Thr Ile  
 410 415 420  
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 Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val Glu Asn Gln Ile Met  
 425 430 435  
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 1459  
 Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala Ile Val Ile Leu Asp  
 440 445 450  
 gaa gca acg gct gaa tca ggc tct gat cat gca aaa cag ctt gaa gat  
 1507  
 Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala Lys Gln Leu Glu Asp  
 455 460 465

gca gcc ctt aaa gtc act gaa aac aga tca gcc atc atc gtg gct cac  
1555

Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His  
470 475 480 485

cgc ctc aac caa gcg aaa acc gcc gat cgc atc atc gtc atg gac tcc  
1603

Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser  
490 495 500

gga gaa atc ata gaa tct gga acc cat gaa gag ctt cga gcg atc ggc  
1651

Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly  
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ggc cga tat gaa caa ctg tgg act gcg tgg tct gcg cgc taattagcca  
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Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser Ala Arg  
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<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

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35 40 45

Ala Ile Ala Gly Leu Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu  
50 55 60

Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg  
65 70 75 80

Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val  
85 90 95

Pro Leu Met Val Gln Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly  
100 105 110

Met Ala Ala Val Asp Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile  
115 120 125

Pro Leu Tyr Trp Thr Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro  
130 135 140

Leu Tyr Thr Arg Glu Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu  
145 150 155 160

Val Gly Ala Val Glu Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu  
 165 170 175  
 Asp Thr Glu Leu Lys Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp  
 180 185 190  
 Ile Ser Ile Ser Val Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn  
 195 200 205  
 Asn Arg Ala Glu Cys Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe  
 210 215 220  
 Tyr Leu Val Asn Ile Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala  
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 Ala Leu Ile Phe His Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly  
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 260 265 270  
 Gly Val Ile Asn Ala Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala  
 275 280 285  
 Ser Ala Ser Thr Ala Leu Thr Leu Phe Asp Val Ser His His Tyr His  
 290 295 300  
 Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu  
 305 310 315 320  
 His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala  
 325 330 335  
 Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu  
 340 345 350  
 Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys  
 355 360 365  
 Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu  
 370 375 380  
 Asp Asn Leu Arg Ile Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His  
 385 390 395 400  
 Ala Val Leu Ala Asp Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln  
 405 410 415  
 Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val  
 420 425 430  
 Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala  
 435 440 445  
 Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala  
 450 455 460  
 Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala  
 465 470 475 480  
 Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile

485										490					495					
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Ala	Arg																			
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catgagtgaacacatacgtgtctgagaaaag tccaggagtg															atg	gct	agc	gga	gcg	115
															Met	Ala	Ser	Gly	Ala	
															1				5	
gag ctg att cgt gcc gcc gac att caa acg gcg cag gca cga att tcc															163					
Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala Gln Ala Arg Ile Ser																				
															10	15	20			
tcc gtc att gca cca act cca ttg cag tat tgc cct cgt ctt tct gag															211					
Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu																				
															25	30	35			
gaa acc gga gcg gaa atc tac ctt aag cgt gag gat ctg cag gat gtt															259					
Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val																				
															40	45	50			
cgt tcc tac aag atc cgc ggt gcg ctg aac tct gga gcg cag ctc acc															307					
Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser Gly Ala Gln Leu Thr																				
															55	60	65			
caa gag cag cgc gat gca ggt atc gtt gcc gca tct gca ggt aac cat															355					
Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His																				
															70	75	80		85	
gcc cag ggc gtg gcc tat gtg tgc aag tcc ttg ggc gtt cag gga cgc															403					
Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu Gly Val Gln Gly Arg																				
															90	95	100			
atc tat gtt cct gtg cag act cca aag caa aag cgt gac cgc atc atg															451					
Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met																				
															105	110	115			
gtt cac ggc gga gag ttt gtc tcc ttg gtg gtc act ggc aat aac ttc															499					
Val His Gly Gly Glu Phe Val Ser Leu Val Val Thr Gly Asn Asn Phe																				
															120	125	130			

gac gaa gca tgc gct gca gcg cat gaa gat gca gag cgc acc ggc gca	547
Asp Glu Ala Ser Ala Ala His Glu Asp Ala Glu Arg Thr Gly Ala	
135 140 145	
acg ctg atc gag cct ttc gat gct cgc aac acc gtc atc ggt cag ggc	595
Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr Val Ile Gly Gln Gly	
150 155 160 165	
acc gtg gct gct gag atc ttg tgc cag ctg act tcc atg ggc aag agt	643
Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr Ser Met Gly Lys Ser	
170 175 180	
gca gat cac gtg atg gtt cca gtc ggc ggt ggc gga ctt ctt gca ggt	691
Ala Asp His Val Met Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly	
185 190 195	
gtg gtc agc tac atg gct gat atg gca cct cgc act gcg atc gtt ggt	739
Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly	
200 205 210	
atc gaa cca gcg gga gca gca tcc atg cag gct gca ttg cac aat ggt	787
Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala Ala Leu His Asn Gly	
215 220 225	
gga cca atc act ttg gag act gtt gat ccc ttt gtg gac ggc gca gca	835
Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe Val Asp Gly Ala Ala	
230 235 240 245	
gtc aaa cgt gtc gga gat ctc aac tac acc atc gtg gag aag aac cag	883
Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile Val Glu Lys Asn Gln	
250 255 260	
ggt cgc gtg cac atg atg agc gcg acc gag ggc gct gtg tgt act gag	931
Gly Arg Val His Met Met Ser Ala Thr Glu Gly Ala Val Cys Thr Glu	
265 270 275	
atg ctc gat ctt tac caa aac gaa ggc atc atc gcg gag cct gct ggc	979
Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile Ala Glu Pro Ala Gly	
280 285 290	
gcg ctg tct atc gct ggg ttg aag gaa atg tcc ttt gca gct cgc tct	
1027	
Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser Phe Ala Ala Arg Ser	
295 300 305	
gtc gtg gtg tgc atc atc tct ggt ggc aac aac gat gtg ctg cgt tat	
1075	
Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr	
310 315 320 325	
gcg gaa atc gct gag cgc tcc ttg gtg cgc cgc ggt tta aag cac tac	
1123	
Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg Gly Leu Lys His Tyr	
330 335 340	
ttc ttg gtg aac ttc ccg caa aag cct ggt cag ttg cgt cac ttc ctg	
1171	
Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln Leu Arg His Phe Leu	
345 350 355	

gaa gat atc ctg gga ccg gat gat gac atc acg ctg ttt gag tac ctc  
1219

Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu  
360 365 370

aag cgc aac aac cgt gag acc ggt act gcg ttg gtg ggt att cac ttg  
1267

Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu Val Gly Ile His Leu  
375 380 385

agt gaa gca tca gga ttg gat tct ttg ctg gaa cgt atg gag gaa tcg  
1315

Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu Arg Met Glu Glu Ser  
390 395 400 405

gca att gat tcc cgt cgc ctc gag ccg ggc acc cct gag tac gaa tac  
1363

Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr Pro Glu Tyr Glu Tyr  
410 415 420

ttg acc taaacatagc tgaaggccac ctc  
1392

Leu Thr

<210> 258

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Ala Ser Gly Ala Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala  
1 5 10 15

Gln Ala Arg Ile Ser Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys  
20 25 30

Pro Arg Leu Ser Glu Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu  
35 40 45

Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser  
50 55 60

Gly Ala Gln Leu Thr Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala  
65 70 75 80

Ser Ala Gly Asn His Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu  
85 90 95

Gly Val Gln Gly Arg Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys  
100 105 110

Arg Asp Arg Ile Met Val His Gly Gly Glu Phe Val Ser Leu Val Val  
115 120 125

Thr Gly Asn Asn Phe Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala  
130 135 140

Glu Arg Thr Gly Ala Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr  
145 150 155 160

Val Ile Gly Gln Gly Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr  
 165 170 175  
 Ser Met Gly Lys Ser Ala Asp His Val Met Val Pro Val Gly Gly Gly  
 180 185 190  
 Gly Leu Leu Ala Gly Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg  
 195 200 205  
 Thr Ala Ile Val Gly Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala  
 210 215 220  
 Ala Leu His Asn Gly Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe  
 225 230 235 240  
 Val Asp Gly Ala Ala Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile  
 245 250 255  
 Val Glu Lys Asn Gln Gly Arg Val His Met Met Ser Ala Thr Glu Gly  
 260 265 270  
 Ala Val Cys Thr Glu Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile  
 275 280 285  
 Ala Glu Pro Ala Gly Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser  
 290 295 300  
 Phe Ala Ala Arg Ser Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn  
 305 310 315 320  
 Asp Val Leu Arg Tyr Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg  
 325 330 335  
 Gly Leu Lys His Tyr Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln  
 340 345 350  
 Leu Arg His Phe Leu Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr  
 355 360 365  
 Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu  
 370 375 380  
 Val Gly Ile His Leu Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu  
 385 390 395 400  
 Arg Met Glu Glu Ser Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr  
 405 410 415  
 Pro Glu Tyr Glu Tyr Leu Thr  
 420

<210> 259  
 <211> 966  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(943)

&lt;223&gt; RXA00766

&lt;400&gt; 259

tatggcgctt gaaccacaaa taaagtctgc accgacgccg gtgatcttaa ttgtcgaacc 60

ctacggcggg tccatccggc aacaaaaccc caacctacca atg gtt ttt tgg gac 115  
Met Val Phe Trp Asp  
1 5

gat gca gcc tta acc cga ggc gat ggc atc ttt gaa aca ctc ctc atc 163  
Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe Glu Thr Leu Leu Ile  
10 15 20

cgc gac gga cat gcc tgc aac gtg cgc cga cac gga gaa cgc ttc aaa 211  
Arg Asp Gly His Ala Cys Asn Val Arg Arg His Gly Glu Arg Phe Lys  
25 30 35

gca tcg gca gca cta ttg gga ctg cca gag ccg atc ctg gaa gac tgg 259  
Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro Ile Leu Glu Asp Trp  
40 45 50

gaa aaa gcc acc caa atg ggc atc gaa tcc tgg tac tcc cac ccc aac 307  
Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp Tyr Ser His Pro Asn  
55 60 65

gca ggc gag gcc tca tgc acc tgg acg ctc agc cga ggt cgt tcc tcc 355  
Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser Arg Gly Arg Ser Ser  
70 75 80 85

acg ggg ctg gcc tca gga tgg tta acc atc acc cca gtc tcc tcc gac 403  
Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr Pro Val Ser Ser Asp  
90 95 100

aaa ctg gcg caa cgt gaa cac ggt gta tcg gtc atg acc agt tca aga 451  
Lys Leu Ala Gln Arg Glu His Gly Val Ser Val Met Thr Ser Ser Arg  
105 110 115

gga tat tcc atc gac acc ggc ctc ccc gga atc gga aaa gcc acc cga 499  
Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile Gly Lys Ala Thr Arg  
120 125 130

ggc gag cta tct aaa gtg gaa cga acc ccc gca cca tgg ctg aca gtc 547  
Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala Pro Trp Leu Thr Val  
135 140 145

ggc gcc aaa aca cta gcc tac gca gca aac atg gca gcc ctg cgc tac 595  
Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met Ala Ala Leu Arg Tyr  
150 155 160 165

gcc aaa tca aac gga ttc gac gat gtg atc ttc acc gat ggc gac cgc 643  
Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe Thr Asp Gly Asp Arg  
170 175 180

gtt cta gaa ggc gcc acc tcc acc gta gtg agt ttc aaa ggc gac aaa 691  
Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser Phe Lys Gly Asp Lys  
185 190 195

atc cgc acc cct tca ccc ggt ggc gac att ctc ccc gga acc acc caa 739  
Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu Pro Gly Thr Thr Gln  
200 205 210



gca gca ctc ttt gca cac gca acc gaa aaa gga tgg cga tgt aaa gaa 787  
 Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly Trp Arg Cys Lys Glu  
 215 220 225  
 aaa gac tta agc att gac gat ctt ttc gga gcc gac agc gtg tgg cta 835  
 Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala Asp Ser Val Trp Leu  
 230 235 240 245  
 gtg tcc tcc gtc cgc gga cca gtt cgg gtg acc agg ctc gat gga cac 883  
 Val Ser Ser Val Arg Gly Pro Val Arg Val Thr Arg Leu Asp Gly His  
 250 255 260  
 aaa tta cgg aaa cca gac aat gaa aaa gaa atc aag gcg ctg att acc 931  
 Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile Lys Ala Leu Ile Thr  
 265 270 275  
 aaa gct ctg ggg tagaggctgg cgctgggact tgc 966  
 Lys Ala Leu Gly  
 280

<210> 260  
 <211> 281  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 260  
 Met Val Phe Trp Asp Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe  
 1 5 10 15  
 Glu Thr Leu Leu Ile Arg Asp Gly His Ala Cys Asn Val Arg Arg His  
 20 25 30  
 Gly Glu Arg Phe Lys Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro  
 35 40 45  
 Ile Leu Glu Asp Trp Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp  
 50 55 60  
 Tyr Ser His Pro Asn Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser  
 65 70 75 80  
 Arg Gly Arg Ser Ser Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr  
 85 90 95  
 Pro Val Ser Ser Asp Lys Leu Ala Gln Arg Glu His Gly Val Ser Val  
 100 105 110  
 Met Thr Ser Ser Arg Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile  
 115 120 125  
 Gly Lys Ala Thr Arg Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala  
 130 135 140  
 Pro Trp Leu Thr Val Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met  
 145 150 155 160  
 Ala Ala Leu Arg Tyr Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe  
 165 170 175  
 Thr Asp Gly Asp Arg Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser

180	185	190
Phe Lys Gly Asp Lys Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu 195 200 205		
Pro Gly Thr Thr Gln Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly 210 215 220		
Trp Arg Cys Lys Glu Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala 225 230 235 240		
Asp Ser Val Trp Leu Val Ser Ser Val Arg Gly Pro Val Arg Val Thr 245 250 255		
Arg Leu Asp Gly His Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile 260 265 270		
Lys Ala Leu Ile Thr Lys Ala Leu Gly 275 280		
<210> 261		
<211> 1224		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(1201)		
<223> RXN01690		
<400> 261		
cctagccatt cctcaaaacc gtgagacgaa attggctatt catcccataa aatggggctg 60		
actagtgtat ctgtcaggta gcagggtgtac cttaaaatcc atg acg tca tta gag 115		
Met Thr Ser Leu Glu 1 5		
ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag 163		
Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys 10 15 20		
gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg 211		
Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met 25 30 35		
gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta 259		
Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu 40 45 50		
gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac 307		
Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His 55 60 65		
tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac 355		
Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp 70 75 80 85		
gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag 403		
Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln 90 95 100		

cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt	451
Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe	
105 110 115	
att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct	499
Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro	
120 125 130	
gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc	547
Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser	
135 140 145	
acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg	595
Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu	
150 155 160 165	
gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct	643
Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro	
170 175 180	
gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga	691
Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly	
185 190 195	
act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc	739
Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala	
200 205 210	
cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat	787
Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Val Trp Leu Asp	
215 220 225	
gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg	835
Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly	
230 235 240 245	
ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt	883
Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu	
250 255 260	
tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta	931
Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val	
265 270 275	
gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc	979
Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr	
280 285 290	
gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct	
1027	
Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala	
295 300 305	
tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct	
1075	
Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala	
310 315 320 325	
cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg	
1123	

His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met  
 330 335 340

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac  
 1171

Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp  
 345 350 355

caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggttttaaga  
 1221

Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly  
 360 365

ccc  
 1224

<210> 262

<211> 367

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser  
 1 5 10 15

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe  
 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp  
 35 40 45

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala  
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala  
 65 70 75 80

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn  
 85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu  
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp  
 115 120 125

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg  
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp  
 145 150 155 160

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr  
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg  
 180 185 190

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala  
 195 200 205

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln  
 210 215 220

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly  
 225 230 235 240

Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu  
 245 250 255

Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys  
 260 265 270

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg  
 275 280 285

Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met  
 290 295 300

Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly  
 305 310 315 320

Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val  
 325 330 335

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln  
 340 345 350

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly  
 355 360 365

&lt;210&gt; 263

&lt;211&gt; 1076

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1053)

&lt;223&gt; FRXA01690

&lt;400&gt; 263

ccc gat cgt ctg aag gaa att ctt gcc gca ccg aag ttc ggt aag ttc 48

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe

1

5

10

15

ttc acc gac cac atg gtg acc att gac tgg aac gag tcg gaa ggc tgg 96

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp

20

25

30

cac aac gcc caa tta gtg cca tac gcg ccg att cct atg gat cct gcc 144

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala

35

40

45

acc acc gta ttc cac tac gga cag gca att ttt gag gga att aag gcc 192

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala

50

55

60

tac cgc cat tcg gac gaa acc atc aag act ttc cgt cct gat gaa aac 240

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn

65	70	75	80	
gcc gag cgt atg cag cgt tca gca gct cga atg gca atg cca cag ttg				288
Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu				
	85	90	95	
cca acc gag gac ttt att aaa gca ctt gaa ctg ctg gta gac gcg gat				336
Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp				
	100	105	110	
cag gat tgg gtt cct gag tac ggc gga gaa gct tcc ctc tac ctg cgc				384
Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg				
	115	120	125	
cca ttc atg atc tcc acc gaa att ggc ttg ggt gtc agc cca gct gat				432
Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp				
	130	135	140	
gcc tac aag ttc ctg gtc atc gca tcc cca gtc ggc gct tac ttc acc				480
Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr				
	145	150	155	160
ggt gga atc aag cct gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc				528
Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg				
	165	170	175	
gct gca ccc ggc gga act ggt gac gcc aaa ttt gct ggc aac tac gcg				576
Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala				
	180	185	190	
gct tct ttg ctt gcc cag tcc cag gct gcg gaa aag ggc tgt gac cag				624
Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln				
	195	200	205	
gtc gta tgg ttg gat gcc atc gag cac aag tac atc gaa gaa atg ggt				672
Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly				
	210	215	220	
ggc atg aac ctt ggg ttc atc tac cgc aac ggc gac caa gtc aag cta				720
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu				
	225	230	235	240
gtc acc cct gaa ctt tcc ggc tca cta ctt cca ggc atc acc cgc aag				768
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys				
	245	250	255	
tca ctt cta caa gta gca cgc gac ttg gga tac gaa gta gaa gag cga				816
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg				
	260	265	270	
aag atc acc acc acc gag tgg gaa gaa gac gca aag tct ggc gcc atg				864
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met				
	275	280	285	
acc gag gca ttt gct tgc ggt act gca gct gtt atc acc cct gtt ggc				912
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly				
	290	295	300	
acc gtg aaa tca gct cac ggc acc ttc gaa gtg aac aac aat gaa gtc				960
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val				
	305	310	315	320

gga gaa atc acg atg aag ctt cgt gaa acc ctc acc gga att cag caa  
1008

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln  
325 330 335

gga aac gtt gaa gac caa aac gga tgg ctt tac cca ctg gtt ggc  
1053

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly  
340 345 350

taaatcaacc ggttttaaga ccc  
1076

<210> 264

<211> 351

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 264

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe  
1 5 10 15

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp  
20 25 30

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala  
35 40 45

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala  
50 55 60

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn  
65 70 75 80

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu  
85 90 95

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp  
100 105 110

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg  
115 120 125

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp  
130 135 140

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr  
145 150 155 160

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg  
165 170 175

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala  
180 185 190

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln  
195 200 205

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly

210	215	220
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu		
225	230	235 240
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys		
	245	250 255
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg		
	260	265 270
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met		
	275	280 285
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly		
	290	295 300
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val		
	305	310 315 320
Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln		
	325	330 335
Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly		
	340	345 350

&lt;210&gt; 265

&lt;211&gt; 1782

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1759)

&lt;223&gt; RXN01026

&lt;400&gt; 265

gaggtgacat ttatgcctct taatagctat actgtcccat gaaacgatat tttaatctca 60

tatagtgaga	tttacagatt	tttaaaggac	ggtgagttcc	atg acc agc ccc gtg	115
				Met Thr Ser Pro Val	
				1 5	

gag aac agc acc tca act gag aag ctg acc ctg gca gag aag gtg tgg	163
Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu Ala Glu Lys Val Trp	
	10 15 20

cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac ctc ctc	211
Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu	
	25 30 35

tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag gca ttt	259
Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe	
	40 45 50

gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa ctg cac	307
Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu Leu His	
	55 60 65

ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag act ggc	355
---	-----



Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys	Thr	Gly		
70					75					80					85		
tca	ctg	ctg	gaa	atc	aac	gac	aag	att	tcc	cgc	ctg	cag	gta	tct	act	403	
Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val	Ser	Thr		
				90					95					100			
ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	atg	ggc	451	
Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	Met	Gly		
			105					110					115				
gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	ggc	gca	499	
Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	Gly	Ala		
		120					125					130					
acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggc	gac	tcc	cac	acc	tcc	acc	547	
Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	Ser	Thr		
		135				140				145							
cac	ggc	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggc	acc	tca	gag	gtt	595	
His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	Glu	Val		
150					155				160					165			
gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	aag	acc	643	
Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	Lys	Thr		
				170				175					180				
atg	gcc	att	gaa	gtt	act	ggc	gaa	ctg	cag	cca	ggc	gtt	tcc	tcc	aag	691	
Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser	Ser	Lys		
			185				190						195				
gac	ctg	att	ctg	gcg	att	atc	gcc	aag	atc	ggc	acc	ggc	ggc	gga	cag	739	
Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly	Gly	Gln		
		200					205					210					
ggc	tac	gtt	ctg	gaa	tac	cgc	ggc	gaa	gca	atc	cgt	aag	atg	tcc	atg	787	
Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met	Ser	Met		
		215				220					225						
gat	gca	cgc	atg	acc	atg	tgc	aac	atg	tcc	atc	gaa	gct	ggc	gca	cgt	835	
Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly	Ala	Arg		
230					235				240					245			
gcc	ggc	atg	atc	gcc	cca	gac	caa	acc	acc	ttc	gac	tac	gtt	gaa	ggc	883	
Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val	Glu	Gly		
				250					255					260			
cgc	gaa	atg	gca	cca	aag	ggc	gcc	gac	tgg	gac	gaa	gca	gtt	gct	tac	931	
Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val	Ala	Tyr		
			265				270						275				
tgg	aag	acc	ctg	cca	acc	gac	gaa	ggc	gca	acc	ttt	gac	aag	gtc	gta	979	
Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys	Val	Val		
		280				285						290					
gaa	atc	gat	ggc	tcg	gca	ctg	acc	cca	ttc	atc	acc	tgg	ggc	acc	aac		
1027																	
Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly	Thr	Asn		
		295				300					305						

cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca gaa gac  
 1075  
 Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro Glu Asp  
 310 315 320 325

ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg cag tac  
 1123  
 Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu Gln Tyr  
 330 335 340

atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc gac acc  
 1171  
 Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr  
 345 350 355

gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg cag atc  
 1219  
 Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Gln Ile  
 360 365 370

gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg cgc atg  
 1267  
 Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met Arg Met  
 375 380 385

atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa gcg ctc  
 1315  
 Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu Ala Leu  
 390 395 400 405

gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt acc gca  
 1363  
 Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg Thr Ala  
 410 415 420

ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag cca ggc  
 1411  
 Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys Pro Gly  
 425 430 435

gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc caa gga  
 1459  
 Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly  
 440 445 450

cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc gcc acc  
 1507  
 Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala Ala Thr  
 455 460 465

gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag gct aga  
 1555  
 Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys Ala Arg  
 470 475 480 485

aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc cac tgc  
 1603  
 Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe His Cys  
 490 495 500

agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct acc tca  
 1651  
 Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser Thr Ser  
                   505                                  510                                  515

agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca act ggc  
 1699  
 Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro Thr Gly  
                   520                                  525                                  530

gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca aga acg  
 1747  
 Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr Arg Thr  
                   535                                  540                                  545

gct ccg ttc tcg tagcaggccc tgactttggc acc  
 1782  
 Ala Pro Phe Ser  
 550

<210> 266  
 <211> 553  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 266  
 Met Thr Ser Pro Val Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu  
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Ala Glu Lys Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly  
                   20                                  25                                  30

Glu Pro Asp Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr  
                   35                                  40                                  45

Ser Pro Gln Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg  
                   50                                  55                                  60

His Pro Glu Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu  
   65                                  70                                  75                                  80

Gly Ile Lys Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg  
                   85                                  90                                  95

Leu Gln Val Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg  
                   100                                  105                                  110

Leu His Pro Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly  
                   115                                  120                                  125

Pro Gln Leu Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp  
                   130                                  135                                  140

Ser His Thr Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile  
 145                                  150                                  155                                  160

Gly Thr Ser Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu  
                   165                                  170                                  175

Lys Pro Phe Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro

			180				185				190				
Gly	Val	Ser	Ser	Lys	Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly
		195					200				205				
Thr	Gly	Gly	Gly	Gln	Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile
		210					215				220				
Arg	Lys	Met	Ser	Met	Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile
		225					230				235		240		
Glu	Ala	Gly	Ala	Arg	Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe
							245		250				255		
Asp	Tyr	Val	Glu	Gly	Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp
			260				265						270		
Glu	Ala	Val	Ala	Tyr	Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr
		275					280				285				
Phe	Asp	Lys	Val	Val	Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile
		290					295				300				
Thr	Trp	Gly	Thr	Asn	Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val
		305					310				315		320		
Pro	Ser	Pro	Glu	Asp	Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu
			325				330						335		
Lys	Ala	Leu	Gln	Tyr	Met	Asp	Leu	Val	Pro	Gly	Thr	Pro	Leu	Arg	Asp
			340				345						350		
Ile	Lys	Ile	Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Ala	Arg	Ile
		355					360				365				
Glu	Asp	Leu	Gln	Ile	Ala	Ala	Asp	Ile	Leu	Lys	Gly	His	Lys	Ile	Ala
		370					375				380				
Asp	Gly	Met	Arg	Met	Met	Val	Val	Pro	Ser	Ser	Thr	Trp	Ile	Lys	Gln
		385					390				395		400		
Glu	Ala	Glu	Ala	Leu	Gly	Leu	Asp	Lys	Ile	Phe	Thr	Asp	Ala	Gly	Ala
			405				410						415		
Glu	Trp	Arg	Thr	Ala	Gly	Cys	Ser	Met	Cys	Leu	Gly	Met	Asn	Pro	Asp
			420				425						430		
Gln	Leu	Lys	Pro	Gly	Glu	Arg	Ser	Ala	Phe	Thr	Ser	Asn	Arg	Asn	Phe
		435					440				445				
Glu	Gly	Arg	Gln	Gly	Pro	Gly	Gly	Arg	Thr	His	Leu	Val	Ser	Pro	Ala
		450					455				460				
Val	Ala	Ala	Ala	Thr	Glu	Ser	Ala	Asp	Pro	Val	Leu	Thr	Cys	Arg	Tyr
		465					470				475		480		
Leu	Arg	Lys	Ala	Arg	Lys	Gln	Trp	Lys	Asn	Leu	Pro	Pro	Thr	Pro	Ala
			485				490						495		
Leu	Ala	Phe	His	Cys	Ser	Asp	Pro	Thr	Trp	Thr	Pro	Thr	Arg	Ser	Ser
			500				505						510		

Gln Pro Ser Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp  
515 520 525

Cys Phe Pro Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro  
530 535 540

Thr Pro Thr Arg Thr Ala Pro Phe Ser  
545 550

<210> 267

<211> 1625

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1) .. (1602)

<223> FRXA01026

<400> 267

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Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp  
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ctc ctc tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag 96  
Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln  
20 25 30

gca ttt gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa 144  
Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu  
35 40 45

ctg cac ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag 192  
Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys  
50 55 60

act ggc tca ctg ctg gaa atc aac gac aag att tcc cgc ctg cag gta 240  
Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val  
65 70 75 80

tct act ctg cgc gac aac tgt gaa gaa ttc ggc gtg cgc ctg cac cca 288  
Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro  
85 90 95

atg ggt gat gtc cga cag ggc atc gtg cac acc gtc ggc cca cag ctc 336  
Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu  
100 105 110

ggc gca acc cag cca ggc atg acc att gtg tgc ggt gac tcc cac acc 384  
Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr  
115 120 125

tcc acc cac ggt gct ttt ggc tcc atg gca ttc ggc atc ggt acc tca 432  
Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser  
130 135 140

gag gtt gag cac gtc atg gct act caa acc ctg cca ctg aag cct ttc 480  
Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe  
145 150 155 160

aag acc atg gcc att gaa gtt act ggt gaa ctg cag cca ggt gtt tcc Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser	528
165 170 175	
tcc aag gac ctg att ctg gcg att atc gcc aag atc ggc acc ggc ggc Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly	576
180 185 190	
gga cag ggc tac gtt ctg gaa tac cgc ggc gaa gca atc cgt aag atg Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met	624
195 200 205	
tcc atg gat gca cgc atg acc atg tgc aac atg tcc atc gaa gct ggc Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly	672
210 215 220	
gca cgt gcc ggc atg atc gcc cca gac caa acc acc ttc gac tac gtt Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val	720
225 230 235 240	
gaa ggc cgc gaa atg gca cca aag ggc gcc gac tgg gac gaa gca gtt Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val	768
245 250 255	
gct tac tgg aag acc ctg cca acc gac gaa ggc gca acc ttt gac aag Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys	816
260 265 270	
gtc gta gaa atc gat ggc tcg gca ctg acc cca ttc atc acc tgg ggc Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly	864
275 280 285	
acc aac cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro	912
290 295 300	
gaa gac ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu	960
305 310 315 320	
cag tac atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc 1008 Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile	
325 330 335	
gac acc gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg 1056 Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu	
340 345 350	
cag atc gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg 1104 Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met	
355 360 365	
cgc atg atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa 1152 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu	
370 375 380	

gcg ctc gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt  
 1200  
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg  
 385 390 395 400

acc gca ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag  
 1248  
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys  
 405 410 415

cca ggc gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc  
 1296  
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg  
 420 425 430

caa gga cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc  
 1344  
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala  
 435 440 445

gcc acc gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag  
 1392  
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys  
 450 455 460

gct aga aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc  
 1440  
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe  
 465 470 475 480

cac tgc agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct  
 1488  
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser  
 485 490 495

acc tca agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca  
 1536  
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro  
 500 505 510

act ggc gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca  
 1584  
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr  
 515 520 525

aga acg gct ccg ttc tcg tagcaggccc tgactttggc acc  
 1625  
 Arg Thr Ala Pro Phe Ser  
 530

<210> 268

<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp  
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Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln

20				25				30							
Ala	Phe	Asp	Gly	Leu	Arg	Met	Thr	Gly	Arg	Lys	L u	Arg	His	Pro	Glu
		35					40					45			
Leu	His	Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys
	50					55					60				
Thr	Gly	Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val
65					70					75					80
Ser	Thr	Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro
				85					90					95	
Met	Gly	Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu
			100					105					110		
Gly	Ala	Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr
			115				120					125			
Ser	Thr	His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser
	130					135					140				
Glu	Val	Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe
145					150					155					160
Lys	Thr	Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser
				165					170					175	
Ser	Lys	Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly
			180					185					190		
Gly	Gln	Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met
		195					200					205			
Ser	Met	Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly
	210					215					220				
Ala	Arg	Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val
225					230					235					240
Glu	Gly	Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val
				245					250					255	
Ala	Tyr	Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys
			260					265					270		
Val	Val	Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly
		275					280					285			
Thr	Asn	Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val	Pro	Ser	Pro
	290					295					300				
Glu	Asp	Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu	Lys	Ala	Leu
305					310					315					320
Gln	Tyr	Met	Asp	Leu	Val	Pro	Gly	Thr	Pro	Leu	Arg	Asp	Ile	Lys	Ile
				325					330					335	
Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Ala	Arg	Ile	Glu	Asp	Leu
			340					345					350		



Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met  
 355 360 365  
 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu  
 370 375 380  
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg  
 385 390 395 400  
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys  
 405 410 415  
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg  
 420 425 430  
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala  
 435 440 445  
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys  
 450 455 460  
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe  
 465 470 475 480  
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser  
 485 490 495  
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro  
 500 505 510  
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr  
 515 520 525  
 Arg Thr Ala Pro Phe Ser  
 530

<210> 269  
 <211> 1143  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
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 <222> (101)..(1120)  
 <223> RXN01127

<400> 269  
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 cactagtga gtccatatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115  
 Met Lys Leu Ala Val  
 1 5  
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163  
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys  
 10 15 20  
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211  
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu

25								30								35								
ggc	gca	cgc	cgt	tac	ctc	aaa	aat	ggc	gag	ctg	ctc	acc	gac	gag	gat									259
Gly	Ala	Arg	Arg	Tyr	Leu	Lys	Asn	Gly	Glu	Leu	Leu	Thr	Asp	Glu	Asp									
		40					45					50												
ctg	gca	tcc	ctg	cgc	gag	cat	gac	gcg	atc	ctt	ctt	ggc	gct	atc	ggc									307
Leu	Ala	Ser	Leu	Arg	Glu	His	Asp	Ala	Ile	Leu	Leu	Gly	Ala	Ile	Gly									
		55				60					65													
gca	cca	ggc	tcc	gtc	cct	cca	gga	att	ctc	gag	cgt	ggc	ttg	ctg	ctg									355
Ala	Pro	Gly	Ser	Val	Pro	Pro	Gly	Ile	Leu	Glu	Arg	Gly	Leu	Leu	Leu									
	70				75					80					85									
aag	atg	cga	ttc	gca	ctg	gat	cac	cac	gtg	aac	ctg	cgc	cca	tcc	aag									403
Lys	Met	Arg	Phe	Ala	Leu	Asp	His	His	Val	Asn	Leu	Arg	Pro	Ser	Lys									
				90					95					100										
ctg	tac	gac	ggc	gtg	gag	tcc	cca	ctg	cgt	aac	cca	ggc	aag	att	gat									451
Leu	Tyr	Asp	Gly	Val	Glu	Ser	Pro	Leu	Arg	Asn	Pro	Gly	Lys	Ile	Asp									
			105					110					115											
ttc	gtt	gtg	gtc	cgc	gaa	ggc	acc	gaa	ggc	gcc	tac	act	ggc	aac	ggc									499
Phe	Val	Val	Val	Arg	Glu	Gly	Thr	Glu	Gly	Ala	Tyr	Thr	Gly	Asn	Gly									
		120					125					130												
gga	gca	atc	cgc	gtg	gga	acc	cct	cac	gag	att	gcc	aac	gaa	acc	tcc									547
Gly	Ala	Ile	Arg	Val	Gly	Thr	Pro	His	Glu	Ile	Ala	Asn	Glu	Thr	Ser									
		135				140					145													
gtg	aac	act	cgc	tac	ggc	gct	gag	cgc	gtt	att	cgc	tac	gca	ttc	gag									595
Val	Asn	Thr	Arg	Tyr	Gly	Ala	Glu	Arg	Val	Ile	Arg	Tyr	Ala	Phe	Glu									
	150				155				160					165										
ctg	gca	cag	agc	cgc	cgc	aag	aag	ctc	acc	ctc	gtg	cac	aag	acc	aac									643
Leu	Ala	Gln	Ser	Arg	Arg	Lys	Lys	Leu	Thr	Leu	Val	His	Lys	Thr	Asn									
				170					175					180										
gtc	ctg	gtt	cac	ggc	ggc	ggc	ctg	tgg	cag	cgc	acc	gta	gat	gag	gtt									691
Val	Leu	Val	His	Gly	Gly	Gly	Leu	Trp	Gln	Arg	Thr	Val	Asp	Glu	Val									
			185					190					195											
gca	aag	gaa	tac	cca	gag	gta	gcc	gtc	gat	tac	aac	cac	atc	gat	gca									739
Ala	Lys	Glu	Tyr	Pro	Glu	Val	Ala	Val	Asp	Tyr	Asn	His	Ile	Asp	Ala									
		200					205					210												
gca	acc	atc	tat	ctg	gtc	act	gat	cct	tcc	cgc	ttc	gat	gtg	att	gtt									787
Ala	Thr	Ile	Tyr	Leu	Val	Thr	Asp	Pro	Ser	Arg	Phe	Asp	Val	Ile	Val									
		215				220					225													
acc	gat	aac	ctc	ttc	ggc	gac	atc	ctc	acc	gat	gag	gca	ggc	gca	gtc									835
Thr	Asp	Asn	Leu	Phe	Gly	Asp	Ile	Leu	Thr	Asp	Glu	Ala	Gly	Ala	Val									
	230				235					240				245										
tct	ggc	gga	att	ggc	ctc	gca	gca	tcc	ggc	aac	atc	gat	gcc	acg	ggc									883
Ser	Gly	Gly	Ile	Gly	Leu	Ala	Ala	Ser	Gly	Asn	Ile	Asp	Ala	Thr	Gly									
				250					255				260											
acc	aac	cct	tcc	atg	ttc	gag	cca	gtc	cac	ggc	tct	gca	cca	gat	atc									931
Thr	Asn	Pro	Ser	Met	Phe	Glu	Pro	Val	His	Gly	Ser	Ala	Pro	Asp	Ile									
			265					270					275											

gca ggc cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg 979  
 Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala  
           280                                  285                                  290

atg ctg ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa  
 1027  
 Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu  
           295                                  300                                  305

aca gcc atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att  
 1075  
 Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile  
           310                                  315                                  320                                  325

tct acc act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc  
 1120  
 Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser  
                                   330                                  335                                  340

taaatttcaa cgccgacccc ctt  
 1143

<210> 270

<211> 340

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 270

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr  
       1                                  5                                  10                                  15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr  
           20                                  25                                  30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu  
           35                                  40                                  45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu  
           50                                  55                                  60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu  
           65                                  70                                  75                                  80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn  
                                   85                                  90                                  95

Leu Arg Pro Ser Lys Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn  
           100                                  105                                  110

Pro Gly Lys Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala  
           115                                  120                                  125

Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile  
           130                                  135                                  140

Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile  
           145                                  150                                  155                                  160

Arg Tyr Ala Phe Glu Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu

[illegible]

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<210> 271
<211> 403
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(403)
<223> FRXA01132
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<400> 271
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cactagtgaa gtccatatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115
Met Lys Leu Ala Val
1 5
att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
10 15 20
gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu
25 30 35

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ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259  
 Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp  
           40                          45                          50

ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt 307  
 Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly  
           55                          60                          65

gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg 355  
 Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu  
           70                          75                          80                          85

aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403  
 Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys  
                           90                          95                          100

<210> 272

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr  
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Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr  
           20                          25                          30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu  
           35                          40                          45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu  
           50                          55                          60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu  
           65                          70                          75                          80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn  
                           85                          90                          95

Leu Arg Pro Ser Lys  
                           100

<210> 273

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXN00536

<400> 273

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tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115  
   Met Ser Pro Asn Asp  
   1                          5

gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc	163
Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg	
10 15 20	
aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc 883  
 Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser  
 250 255 260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg 931  
 Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu  
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979  
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu  
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc  
 1027  
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly  
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac  
 1075  
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn  
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc  
 1123  
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg  
 330 335 340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag  
 1171  
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu  
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc  
 1219  
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser  
 360 365 370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt  
 1267  
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val  
 375 380 385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac  
 1315  
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp  
 390 395 400 405

acc cga atg gga ggt tcc tta cct gcc tat cga tcc aaa gga tgt cgg  
 1363  
 Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg Ser Lys Gly Cys Arg  
 410 415 420

tcg cga cta cga ggc tgt tat ccg cgt gaa ctc cca gtc cgg caa ggg  
 1411  
 Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly  
 425 430 435

cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg  
 1459  
 Arg Arg Cys Leu His His Glu Asp Arg Ser Arg Ser Ala Asp Pro Ser  
 440 445 450

ctc cat gca ggt tgagttctcc accgttgtcc aga

1494

Leu His Ala Gly

455

<210> 274

<211> 457

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 274

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr  
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Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg  
20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val  
35 40 45

Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr  
50 55 60

Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala  
65 70 75 80

Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu  
85 90 95

Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala  
100 105 110

Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met  
115 120 125

Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His  
130 135 140

Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile  
145 150 155 160

Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe  
165 170 175

Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu  
180 185 190

Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp  
195 200 205

Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys  
210 215 220

Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn  
225 230 235 240

Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn  
245 250 255



Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg  
 260 265 270

Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly  
 275 280 285

Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu  
 290 295 300

Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val  
 305 310 315 320

Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp  
 325 330 335

Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln  
 340 345 350

Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr  
 355 360 365

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala  
 370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp  
 385 390 395 400

Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg  
 405 410 415

Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu  
 420 425 430

Pro Val Arg Gln Gly Arg Arg Cys Leu His His Glu Asp Arg Ser Arg  
 435 440 445

Ser Ala Asp Pro Ser Leu His Ala Gly  
 450 455

&lt;210&gt; 275

&lt;211&gt; 1333

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1333)

&lt;223&gt; FRXA00536

&lt;400&gt; 275

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tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115  
 Met Ser Pro Asn Asp  
 1 5

gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc 163  
 Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg  
 10 15 20

aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
ggt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
ggt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	
ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc	883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser	
250 255 260	
att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg	931

Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu  
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979  
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu  
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc  
 1027  
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly  
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac  
 1075  
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn  
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc  
 1123  
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg  
 330 335 340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag  
 1171  
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu  
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc  
 1219  
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser  
 360 365 370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt  
 1267  
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val  
 375 380 385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac  
 1315  
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp  
 390 395 400 405

acc gaa tgg gag gtt cct  
 1333  
 Thr Glu Trp Glu Val Pro  
 410

&lt;210&gt; 276

&lt;211&gt; 411

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 276

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr  
 1 5 10 15

Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg  
 20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val

35					40					45					
Glu	Asp	Ile	Ser	Leu	Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr
50					55					60					
Val	Ala	Pro	Gln	Trp	Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala
65					70					75					80
Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu
				85					90					95	
Leu	Val	Gln	Met	Gly	Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala
			100					105					110		
Ser	Gln	Thr	Asp	Phe	Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met
		115					120					125			
Ile	Pro	Asp	Asp	Val	Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His
	130					135					140				
Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile
145					150					155					160
Val	His	Phe	Tyr	Asn	Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe
				165					170					175	
Arg	Met	Asp	Lys	Val	Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu
			180					185					190		
Leu	Ile	Lys	Thr	Ile	Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp
		195					200					205			
Gln	Tyr	Ser	Pro	Glu	Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys
	210					215					220				
Glu	Val	Val	Asp	Ala	Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn
225					230					235					240
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn
				245					250					255	
Val	Tyr	Ala	Asp	Ser	Ile	Glu	Trp	Met	His	Arg	Asn	Leu	Asn	Arg	Arg
			260					265					270		
Asp	Ser	Ile	Ile	Leu	Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly
		275					280					285			
Val	Gly	Ala	Ala	Glu	Leu	Gly	Tyr	Met	Ala	Gly	Ala	Asp	Arg	Ile	Glu
	290					295					300				
Gly	Cys	Leu	Phe	Gly	Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Cys	Leu	Val
305					310					315					320
Thr	Leu	Ala	Leu	Asn	Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp
				325					330					335	
Phe	Thr	Asp	Ile	Arg	Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln
			340					345					350		
Leu	Arg	Val	Pro	Glu	Arg	His	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Phe	Thr
		355					360					365			

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala  
370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp  
385 390 395 400

Glu Gln Leu Arg Asp Thr Glu Trp Glu Val Pro  
405 410

<210> 277

<211> 714

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(691)

<223> RXN02965

<400> 277

caggaggccg caccacacctg gtatccccag cagtcgcagc cgccaccgaa tccgcggacc 60

ctgtcctcac ctgcagatat ctaaggaagg ctagaaaaca atg gaa aaa ttt acc 115  
Met Glu Lys Phe Thr  
1 5

acc tac acc ggc gtt ggc gtt cca ctg cag cga tcc aac gtg gac acc 163  
Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr  
10 15 20

gac cag atc atc cca gcc gtc tac ctc aag cgc gtc acc cgg acc ggc 211  
Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly  
25 30 35

ttc gaa gac gga ctg ttt tcc aac tgg cgc caa aac gac ccc aac ttt 259  
Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe  
40 45 50

gtc ctc aac acc gac acc tac aag aac ggc tcc gtt ctc gta gca ggc 307  
Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly  
55 60 65

cct gac ttt ggc acc ggc tcc tcc cgc gag cac gcc gtc tgg gca ctc 355  
Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu  
70 75 80 85

atg gac tac ggc ttc cgc gct gtc ttc tcc tca cga ttc gcc gac atc 403  
Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile  
90 95 100

ttc cgc ggc aac tcc gga aaa gcg ggc atg ctc acc ggc atc atg gaa 451  
Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu  
105 110 115

cag tcc gac atc gaa ctt ctg tgg aag ctc atg gaa caa acc cca ggc 499  
Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly  
120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp  
 135 140 145  
 gta gtg atc agc ttc gaa gtt gac ccc tac atc cgc tgg cgt ttg atg 595  
 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met  
 150 155 160 165  
 gaa ggc ctc gac gac gct ggc ctg acc ctg cgc aag ctc gat gaa att 643  
 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile  
 170 175 180  
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691  
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala  
 185 190 195  
 taagtttcag tctgatagcg aaa 714

&lt;210&gt; 278

&lt;211&gt; 197

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 278

Met Glu Lys Phe Thr Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg  
 1 5 10 15  
 Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg  
 20 25 30  
 Val Thr Arg Thr Gly Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln  
 35 40 45  
 Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser  
 50 55 60  
 Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His  
 65 70 75 80  
 Ala Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser  
 85 90 95  
 Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu  
 100 105 110  
 Thr Gly Ile Met Glu Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met  
 115 120 125  
 Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile  
 130 135 140  
 Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile  
 145 150 155 160  
 Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg  
 165 170 175  
 Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys  
 180 185 190  
 Pro Arg Thr Asn Ala

195

<210> 279  
 <211> 936  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(913)  
 <223> RXN01929

&lt;400&gt; 279

aaaatttgac tccataacga gaacttaatc gagcaacacc cctgaacagt gaatcaaac 60

ggaatttatt tattctgagc tggatcatcac atctatactc atg ccc atg tca ggc 115  
 Met Pro Met Ser Gly  
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163  
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val  
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211  
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala  
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259  
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser  
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307  
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu  
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355  
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg  
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403  
 Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro  
 90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451  
 Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala  
 105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499  
 Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg  
 120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547  
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr  
 135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595  
 Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly  
 150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643

Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala  
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691  
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg  
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739  
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly  
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787  
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu  
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835  
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly  
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883  
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala  
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933  
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
 265 270

aag 936

&lt;210&gt; 280

&lt;211&gt; 271

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 280

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe  
 1 5 10 15

Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr  
 20 25 30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu  
 35 40 45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr  
 50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr  
 65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr  
 85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met  
 100 105 110

Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile  
 115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly



130	135	140
His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val 145 150 155 160		
Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg 165 170 175		
Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro 180 185 190		
Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile 195 200 205		
Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln 210 215 220		
Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu 225 230 235 240		
Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile 245 250 255		
Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe 260 265 270		

&lt;210&gt; 281

&lt;211&gt; 930

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(907)

&lt;223&gt; FRXA01929

&lt;400&gt; 281

tgactccata acgagaactt aatcgagcaa caccctgaa cagtgaatca aatcggaatt 60

tatttattct gagctgggtca tcacatctat actcatgccc atg tca ggc att gat	115
Met Ser Gly Ile Asp	
1 5	

gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly	
10 15 20	

cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile	
25 30 35	

ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Ser Ala Ala	
40 45 50	

aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu	
55 60 65	

atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355
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Met	Ile	Val	Leu	Ala	Lys	Ala	Val	Thr	Ile	Ala	Thr	Lys	Arg	Ala	Leu		
70					75					80					85		
gtg	gtg	gtt	gat	ctg	ccg	ttt	ggg	acc	tat	gag	gtg	agc	cca	aat	cag	403	
Val	Val	Val	Asp	Leu	Pro	Phe	Gly	Thr	Tyr	Glu	Val	Ser	Pro	Asn	Gln		
				90				95						100			
gcg	gtg	gag	tcc	gcg	atc	cgg	gtc	atg	cgt	gaa	acg	ggg	gcg	gct	gcg	451	
Ala	Val	Glu	Ser	Ala	Ile	Arg	Val	Met	Arg	Glu	Thr	Gly	Ala	Ala	Ala		
			105					110					115				
gtg	aag	atc	gag	ggg	ggc	gtg	gag	atc	gcg	cag	acg	att	cga	cgc	att	499	
Val	Lys	Ile	Glu	Gly	Gly	Val	Glu	Ile	Ala	Gln	Thr	Ile	Arg	Arg	Ile		
		120					125					130					
gtt	gat	gct	gga	att	ccg	gtt	gtc	ggc	cac	atc	ggg	tac	acc	ccg	cag	547	
Val	Asp	Ala	Gly	Ile	Pro	Val	Val	Gly	His	Ile	Gly	Tyr	Thr	Pro	Gln		
	135					140				145							
tcc	gag	cat	tcc	ttg	ggc	ggc	cac	gtg	gtt	cag	ggg	cgt	ggc	gcg	agt	595	
Ser	Glu	His	Ser	Leu	Gly	Gly	His	Val	Val	Gln	Gly	Arg	Gly	Ala	Ser		
150					155					160					165		
tct	gga	aag	ctc	atc	gcc	gat	gcc	cgc	gcg	ttg	gag	cag	gcg	ggg	gcg	643	
Ser	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Arg	Ala	Leu	Glu	Gln	Ala	Gly	Ala		
			170					175						180			
ttt	gcg	gtt	gtg	ttg	gag	atg	gtt	cca	gca	gag	gca	gcg	cgc	gag	gtt	691	
Phe	Ala	Val	Val	Leu	Glu	Met	Val	Pro	Ala	Glu	Ala	Ala	Arg	Glu	Val		
			185					190					195				
acc	gag	gat	ctt	tcc	atc	acc	act	atc	gga	atc	ggg	gcc	ggc	aat	ggc	739	
Thr	Glu	Asp	Leu	Ser	Ile	Thr	Thr	Ile	Gly	Ile	Gly	Ala	Gly	Asn	Gly		
		200					205					210					
aca	gat	ggg	cag	gtt	ttg	gtg	tgg	cag	gat	gcc	ttc	ggc	ctc	aac	cgc	787	
Thr	Asp	Gly	Gln	Val	Leu	Val	Trp	Gln	Asp	Ala	Phe	Gly	Leu	Asn	Arg		
	215					220					225						
ggc	aag	aag	cca	cgc	ttc	gtc	cgc	gag	tac	gcc	acc	ttg	ggc	gat	tcc	835	
Gly	Lys	Lys	Pro	Arg	Phe	Val	Arg	Glu	Tyr	Ala	Thr	Leu	Gly	Asp	Ser		
230					235					240					245		
ttg	cac	gac	gcc	gcg	cag	gcc	tac	atc	gcc	gat	atc	cac	gcg	ggg	acc	883	
Leu	His	Asp	Ala	Ala	Gln	Ala	Tyr	Ile	Ala	Asp	Ile	His	Ala	Gly	Thr		
				250				255						260			
ttc	cca	ggc	gaa	gcg	gag	tcc	ttt	taatgcaggt	agcaaccaca	aag						930	
Phe	Pro	Gly	Glu	Ala	Glu	Ser	Phe										
			265														

&lt;210&gt; 282

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 282

Met	Ser	Gly	Ile	Asp	Ala	Lys	Lys	Ile	Arg	Thr	Arg	His	Phe	Arg	Glu
1					5				10					15	

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala  
                   20                                  25                                  30  
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val  
                   35                                  40                                  45  
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser  
                   50                                  55                                  60  
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala  
                   65                                  70                                  75                                  80  
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu  
                                   85                                  90                                  95  
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu  
                                   100                                  105                                  110  
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln  
                   115                                  120                                  125  
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile  
                   130                                  135                                  140  
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln  
                   145                                  150                                  155                                  160  
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu  
                                   165                                  170                                  175  
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu  
                                   180                                  185                                  190  
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile  
                   195                                  200                                  205  
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala  
                   210                                  215                                  220  
 Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala  
                   225                                  230                                  235                                  240  
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp  
                                   245                                  250                                  255  
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe  
                   260                                  265

&lt;210&gt; 283

&lt;211&gt; 1065

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1042)

&lt;223&gt; RXN01420

&lt;400&gt; 283

cgaagttcac gactacaggc attacctggg tgctgatttt gcgcgagtaa agctgtggct 60

gcggaatgcg	ctgctcatcc	acacgtggaa	tcctgattgg	gtg	acg	ctg	ggt	gga	115							
				Val	Thr	Leu	Gly	Gly								
				1				5								
ttg	aat	gta	cca	tcg	tgg	tcg	ctg	ggc	gcg	gaa	atg	ctg	ttc	tac	ctg	163
Leu	Asn	Val	Pro	Ser	Trp	Ser	Leu	Gly	Ala	Glu	Met	Leu	Phe	Tyr	Leu	
				10				15						20		
acg	ttc	ccg	ctg	ttt	att	ccg	tta	gtg	cgc	aaa	gtg	aag	ggc	gtg	ggc	211
Thr	Phe	Pro	Leu	Phe	Ile	Pro	Leu	Val	Arg	Lys	Val	Lys	Gly	Val	Gly	
				25				30					35			
aac	tgg	tgg	gca	ttt	ggc	atc	acc	ttt	gcc	gtg	agc	ctg	gcg	ctg	att	259
Asn	Trp	Trp	Ala	Phe	Gly	Ile	Thr	Phe	Ala	Val	Ser	Leu	Ala	Leu	Ile	
			40				45					50				
aca	gtg	att	cac	ttt	tat	gcg	gac	gga	cca	aag	ggg	att	gag	aac	ttc	307
Thr	Val	Ile	His	Phe	Tyr	Ala	Asp	Gly	Pro	Lys	Gly	Ile	Glu	Asn	Phe	
	55					60					65					
ttt	gtt	cct	cgc	ctg	tgg	gac	acc	aat	gtg	tca	ccg	gtc	gcg	gaa	gtt	355
Phe	Val	Pro	Arg	Leu	Trp	Asp	Thr	Asn	Val	Ser	Pro	Val	Ala	Glu	Val	
	70				75				80					85		
cac	gcc	gat	cca	gtg	tgg	ttt	atg	cag	gaa	gaa	att	ccc	gtg	ctg	gaa	403
His	Ala	Asp	Pro	Val	Trp	Phe	Met	Gln	Glu	Glu	Ile	Pro	Val	Leu	Glu	
				90				95						100		
tct	tac	tgg	ctg	tct	tac	tac	ttc	ccg	ctg	acc	aga	ctc	atc	gag	ttc	451
Ser	Tyr	Trp	Leu	Ser	Tyr	Tyr	Phe	Pro	Leu	Thr	Arg	Leu	Ile	Glu	Phe	
			105					110					115			
tac	ctc	ggt	gtg	ttt	ggc	gcg	aag	ctg	gtt	gct	gaa	ggc	atg	ttt	aaa	499
Tyr	Leu	Gly	Val	Phe	Gly	Ala	Lys	Leu	Val	Ala	Glu	Gly	Met	Phe	Lys	
		120				125					130					
aac	acc	aac	atc	acc	atc	ccg	ctg	atc	gca	ctg	gct	gtt	tct	ttt	gtt	547
Asn	Thr	Asn	Ile	Thr	Ile	Pro	Leu	Ile	Ala	Leu	Ala	Val	Ser	Phe	Val	
	135					140					145					
gct	act	tgg	ttt	gtg	cca	ctg	gca	ttc	aag	atg	tct	gtc	atc	atg	tcc	595
Ala	Thr	Trp	Phe	Val	Pro	Leu	Ala	Phe	Lys	Met	Ser	Val	Ile	Met	Ser	
	150				155				160						165	
ctg	cca	atg	gct	ttt	gtt	gtg	gca	acg	ctt	gcg	gtg	aga	gac	att	gaa	643
Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	Leu	Ala	Val	Arg	Asp	Ile	Glu	
				170				175						180		
ggc	aag	agt	ggg	gaa	atc	gcc	tcg	cct	cgc	gca	gtt	ttg	ttg	ggt	aat	691
Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Arg	Ala	Val	Leu	Leu	Gly	Asn	
			185				190					195				
att	tcc	ttt	gcc	ttc	tac	atg	gtg	caa	ttc	ccc	gtc	atg	gtg	ttt	gtg	739
Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	Phe	Pro	Val	Met	Val	Phe	Val	
		200				205					210					
cag	cgc	tat	ttc	att	gct	ggc	aaa	gaa	tac	ggc	ttc	ctt	ggc	tgg	gca	787
Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	Tyr	Gly	Phe	Leu	Gly	Trp	Ala	
	215				220					225						

ttc tat gca gtg gtg tgt ttc atc gtg tcg gtc att ctc gcg tgg gtg 835  
 Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val  
 230 235 240 245

ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag 883  
 Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys  
 250 255 260

aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg 931  
 Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu  
 265 270 275

aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act 979  
 Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr  
 280 285 290

cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct  
 1027  
 Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala  
 295 300 305

acc gga atc aaa tct tagggaagga aaacatatgg cta  
 1065  
 Thr Gly Ile Lys Ser  
 310

<210> 284

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

Val Thr Leu Gly Gly Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu  
 1 5 10 15

Met Leu Phe Tyr Leu Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys  
 20 25 30

Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val  
 35 40 45

Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys  
 50 55 60

Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser  
 65 70 75 80

Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu  
 85 90 95

Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr  
 100 105 110

Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala  
 115 120 125

Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu  
 130 135 140

Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met

145				150				155				160			
Ser	Val	Ile	Met	Ser	Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	Leu	Ala
165								170				175			
Val	Arg	Asp	Ile	Glu	Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Arg	Ala
180								185				190			
Val	Leu	Leu	Gly	Asn	Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	Phe	Pro
195								200				205			
Val	Met	Val	Phe	Val	Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	Tyr	Gly
210												220			
Phe	Leu	Gly	Trp	Ala	Phe	Tyr	Ala	Val	Val	Cys	Phe	Ile	Val	Ser	Val
225												235			
Ile	Leu	Ala	Trp	Val	Leu	Phe	Thr	Phe	Val	Asp	Asp	Pro	Leu	Met	Lys
												250			
Ala	Thr	Ala	Arg	Lys	Lys	Gly	Ser	Arg	Arg	Leu	Lys	Gln	Ser	Asn	Ile
												260			
Leu	Val	Arg	Asp	Leu	Lys	Val	Leu	Phe	Gly	Lys	Ser	Pro	Glu	Lys	Pro
												275			
Leu	Lys	Val	Glu	Thr	Arg	Ala	Glu	Asn	Leu	Thr	Glu	Asn	Ser	Glu	Ala
												290			
Pro	Ala	Lys	Val	Ala	Thr	Gly	Ile	Lys	Ser						
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												310			

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<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1114)
<223> RXS01145
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cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
Met Ala Ile Glu Leu
1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
Arg Asp Ser Gly Val Glu Val Ile Gly Leu Arg Glu Gly Ser Lys
40 45 50

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tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala 55 60 65	307
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr 70 75 80 85	355
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala 90 95 100	403
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu 105 110 115	451
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly 120 125 130	499
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro 135 140 145	547
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu 150 155 160 165	595
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile 170 175 180	643
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln 185 190 195	691
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu 200 205 210	739
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val 215 220 225	787
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile 230 235 240 245	835
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr 250 255 260	883
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys 265 270 275	931
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile 280 285 290	979

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc  
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser  
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc  
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu  
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac  
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala  
330 335

ccctttgacg gct  
1137

<210> 286

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 286

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly  
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala  
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp  
180 185 190



Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val  
 195 200 205  
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met  
 210 215 220  
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met  
 225 230 235 240  
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala  
 245 250 255  
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr  
 260 265 270  
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe  
 275 280 285  
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu  
 290 295 300  
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala  
 305 310 315 320  
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu  
 325 330 335  
 Thr Ala

<210> 287  
 <211> 556  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(556)  
 <223> FRXA01145

<400> 287  
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 Met Ala Ile Glu Leu  
 1 5  
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163  
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val  
 10 15 20  
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211  
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu  
 25 30 35  
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259  
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys  
 40 45 50  
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala  
 55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355  
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr  
 70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403  
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala  
 90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451  
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu  
 105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499  
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly  
 120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547  
 Pro Gly His Leu Val Arg Gln Phe Val Asp Gly Lys Gly Val Pro  
 135 140 145

tgc ctc atc 556  
 Cys Leu Ile  
 150

&lt;210&gt; 288

&lt;211&gt; 152

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 288

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile  
 1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala  
 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu  
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu  
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu  
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu  
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn  
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met  
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp  
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile  
145 150

<210> 289  
<211> 1350  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1327)  
<223> RXA02375

<400> 289  
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aagcgttcga ttacgggata atctcccaac gccaacccaa atg gcg ccg gtg aca 115  
Met Ala Pro Val Thr  
1 5

ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163  
Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser  
10 15 20

ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211  
Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His  
25 30 35

gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259  
Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val  
40 45 50

aaa att ggt tcg tcc tca ttg act aac gat gag gac gga cac acc gtc 307  
Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val  
55 60 65

gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355  
Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met  
70 75 80 85

gaa gct ggc tcg gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403  
Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala  
90 95 100

gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451  
Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val  
105 110 115

aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499  
Lys Gln Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp  
120 125 130

gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547  
Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu  
135 140 145

acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595  
Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg  
150 155 160 165

acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa 643  
 Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu  
 170 175 180

aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga 691  
 Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg  
 185 190 195

ctt gct gca att gtg gcg cac ctg gtg tcg gct gat gct ttg gtg ctg 739  
 Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu  
 200 205 210

ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc 787  
 Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr  
 215 220 225

gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc 835  
 Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val  
 230 235 240 245

att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag 883  
 Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys  
 250 255 260

gtg tct gct gca cgt ttg gct tcc cga agt ggc gtg cct gtg ctg ttg 931  
 Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu  
 265 270 275

acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc 979  
 Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly  
 280 285 290

act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg  
 1027  
 Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp  
 295 300 305

gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc  
 1075  
 Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly  
 310 315 320 325

gcg gtg gaa gca gtg acc tcc ggt ggt aaa tct ttg ctg gct gtg ggc  
 1123  
 Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly  
 330 335 340

att act gaa atc att ggt gat ttc cag cag ggt gag atc gtg gag atc  
 1171  
 Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile  
 345 350 355

ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat  
 1219  
 Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp  
 360 365 370

tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca  
 1267  
 Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln Thr Gln Asp Leu Pro  
 375 380 385

gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac  
1315

Asp Gly Met Gln Arg Pro Val Val His Ala Asp Tyr Leu Ser Asn Tyr  
390 395 400 405

gcc agc cgc gcg taaagcgcgg gcctgctggt ggc  
1350

Ala Ser Arg Ala

<210> 290

<211> 409

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 290

Met Ala Pro Val Thr Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala  
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Ser Ile Gly Ala Ser Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser  
20 25 30

Ala Ala Tyr Gly His Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala  
35 40 45

Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu  
50 55 60

Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala  
65 70 75 80

Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser  
85 90 95

Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro  
100 105 110

Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Ala Val Gly Gln Val His  
115 120 125

Leu Met His Gln Trp Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile  
130 135 140

Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala  
145 150 155 160

Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val  
165 170 175

Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe  
180 185 190

Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala  
195 200 205

Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn  
210 215 220

Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn

225				230				235				240			
Asp	Leu	Lys	Gly	Val	Ile	Ala	Gly	Asp	Gly	Gly	Lys	Val	Gly	Thr	Gly
245				250				255							
Gly	Met	Ala	Ser	Lys	Val	Ser	Ala	Ala	Arg	Leu	Ala	Ser	Arg	Ser	Gly
260				265				270							
Val	Pro	Val	Leu	Leu	Thr	Ser	Ala	Ala	Asn	Ile	Gly	Pro	Ala	Leu	Glu
275				280				285							
Asp	Ala	Gln	Val	Gly	Thr	Val	Phe	His	Pro	Lys	Asp	Asn	Arg	Leu	Ser
290				295				300							
Ala	Trp	Lys	Phe	Trp	Ala	Leu	Tyr	Ala	Ala	Asp	Thr	Ala	Gly	Lys	Ile
305				310				315				320			
Arg	Leu	Asp	Asp	Gly	Ala	Val	Glu	Ala	Val	Thr	Ser	Gly	Gly	Lys	Ser
325				330				335							
Leu	Leu	Ala	Val	Gly	Ile	Thr	Glu	Ile	Ile	Gly	Asp	Phe	Gln	Gln	Gly
340				345				350							
Glu	Ile	Val	Glu	Ile	Leu	Gly	Pro	Ala	Gly	Gln	Ile	Ile	Gly	Arg	Gly
355				360				365							
Glu	Val	Ser	Tyr	Asp	Ser	Asp	Thr	Leu	Gln	Ser	Met	Val	Gly	Met	Gln
370				375				380							
Thr	Gln	Asp	Leu	Pro	Asp	Gly	Met	Gln	Arg	Pro	Val	Val	His	Ala	Asp
385				390				395				400			
Tyr	Leu	Ser	Asn	Tyr	Ala	Ser	Arg	Ala							
405															

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<210> 291 .
<211> 1419
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1396)  
<223> RXN02382
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<400> 291
gagcagatgg ccaccgaggt cgatgtgggtg gctggctact aggcctttta tgggtgtgatc 60
cgacactgtt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
Met Ser Ser Thr Thr
1 5
cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
10 15 20
aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
25 30 35

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acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt	259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val	
40 45 50	
gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg	307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala	
55 60 65	
ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt	355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu	
70 75 80 85	
gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct	403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala	
90 95 100	
ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa	451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu	
105 110 115	
aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc	499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly	
120 125 130	
atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg	547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu	
135 140 145	
gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct	595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala	
150 155 160 165	
gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gtc ctc gag	643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu	
170 175 180	
cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg cct tgc caa acc	691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Pro Cys Gln Thr	
185 190 195	
cgc gga tcc gtc caa gat ttg atc acc gca cgc ggc ctc gtt gac gtg	739
Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg Gly Leu Val Asp Val	
200 205 210	
gtc atc cca cgc ggc ggc gca gga cta atc aac gca gtg gtc acc ggt	787
Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn Ala Val Val Thr Gly	
215 220 225	
gcg acc gtg ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac	835
Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr	
230 235 240 245	
atc gat gcc gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac	883
Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn	
250 255 260	
ggc aag acc cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt	931
Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu	
265 270 275	
ctc gac gcc gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg	979

Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala  
 280 285 290

ctc cag gaa gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa  
 1027

Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu  
 295 300 305

gca ttc ggt gca acc gac gtg gtg gaa gca act gaa act gac tgg gat  
 1075

Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp  
 310 315 320 325

tct gag tac ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg  
 1123

Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val  
 330 335 340

gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa  
 1171

Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu  
 345 350 355

gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc  
 1219

Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg  
 360 365 370

gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat  
 1267

Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp  
 375 380 385

ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa  
 1315

Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys  
 390 395 400 405

ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag  
 1363

Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys  
 410 415 420

tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca  
 1416

Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro  
 425 430

agc  
 1419

<210> 292

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg  
 1 5 10 15



Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp  
 20 25 30  
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala  
 35 40 45  
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala  
 50 55 60  
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile  
 65 70 75 80  
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly  
 85 90 95  
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg  
 100 105 110  
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro  
 115 120 125  
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val  
 130 135 140  
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg  
 145 150 155 160  
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu  
 165 170 175  
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu  
 180 185 190  
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg  
 195 200 205  
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn  
 210 215 220  
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly  
 225 230 235 240  
 Asn Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile  
 245 250 255  
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala  
 260 265 270  
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu  
 275 280 285  
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg  
 290 295 300  
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr  
 305 310 315 320  
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala  
 325 330 335  
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser

340	345	350
Thr Lys His Thr Glu Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln		
355	360	365
Arg Phe Ala Asp Arg Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser		
370	375	380
Thr Ala Tyr Thr Asp Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly		
385	390	395
Ile Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu		
405	410	415
Leu Thr Ser Thr Lys Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro		
420	425	430

<210> 293  
 <211> 724  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(709)  
 <223> FRXA02378

<400> 293  
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cgacactggt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115  
 Met Ser Ser Thr Thr  
 1 5

cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163  
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala  
 10 15 20

aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211  
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly  
 25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259  
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val  
 40 45 50

gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307  
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala  
 55 60 65

ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355  
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu  
 70 75 80 85

gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403  
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala  
 90 95 100

ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa 451  
 Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu  
 105 110 115  
 aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc 499  
 Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly  
 120 125 130  
 atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg 547  
 Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu  
 135 140 145  
 gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595  
 Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala  
 150 155 160 165  
 gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gta ctc gag 643  
 Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu  
 170 175 180  
 cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691  
 Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro  
 185 190 195  
 gcg gat ccg tcc aag att tgatcaccgg acgcg 724  
 Ala Asp Pro Ser Lys Ile  
 200

&lt;210&gt; 294

&lt;211&gt; 203

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 294

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg  
 1 5 10 15  
 Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp  
 20 25 30  
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala  
 35 40 45  
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala  
 50 55 60  
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile  
 65 70 75 80  
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly  
 85 90 95  
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg  
 100 105 110  
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro  
 115 120 125  
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val

130                      135                      140  
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg  
 145                      150                      155                      160  
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu  
                     165                      170                      175  
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu  
                     180                      185                      190  
 Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile  
                     195                      200

&lt;210&gt; 295

&lt;211&gt; 623

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(600)

&lt;223&gt; FRXA02382

&lt;400&gt; 295

ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac atc gat gcc 48  
 Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala  
     1                    5                    10                    15  
 gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac ggc aag acc 96  
 Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr  
                     20                    25                    30  
 cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc 144  
 Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala  
                     35                    40                    45  
 gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa 192  
 Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu  
     50                    55                    60  
 gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa gca ttc ggt 240  
 Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly  
     65                    70                    75                    80  
 gca acc gac gtg gtg gaa gca act gaa act gac tgg gat tct gag tac 288  
 Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr  
                     85                    90                    95  
 ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct 336  
 Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala  
                     100                    105                    110  
 ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc 384  
 Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala  
                     115                    120                    125  
 acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca 432  
 Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala  
     130                    135                    140

gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480  
 Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln  
 145 150 155 160

tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528  
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala  
 165 170 175

cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576  
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu  
 180 185 190

cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca agc 623  
 Gln Gly Thr Gly Gln Ile Arg Pro  
 195 200

&lt;210&gt; 296

&lt;211&gt; 200

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 296

Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala  
 1 5 10 15

Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr  
 20 25 30

Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala  
 35 40 45

Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu  
 50 55 60

Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly  
 65 70 75 80

Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr  
 85 90 95

Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala  
 100 105 110

Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala  
 115 120 125

Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala  
 130 135 140

Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln  
 145 150 155 160

Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala  
 165 170 175

Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu  
 180 185 190

Gln Gly Thr Gly Gln Ile Arg Pro

195

200

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<210> 297
<211> 933
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(910)  
<223> RXA02499
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**<400> 297**

cctgggtcatg acgttcgggc cgctggcaat cgtcatgtaa tttgtcgttt tgggcccccg 60

ctgctgcaaa acaggggtgg ttagtggcag tgtgggaacc atg aca aca att gct 115  
Met Thr Thr Ile Ala  
1 5

gta atc ggc ggc gga caa atc ggc gag gct tta gtc tca ggt ttg atc 163  
Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu Val Ser Gly Leu Ile  
10 15 20

gcg gcc aac atg aat cca caa aat att cgc gtc acc aac cgt tcg gaa 211  
Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val Thr Asn Arg Ser Glu  
25 30 35

gag cgc ggc caa gag ctg cgt gac cgc tac ggc atc ctc aac atg acg 259  
Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly Ile Leu Asn Met Thr  
40 45 50

gat aat tcc caa gcc gca gac gaa gcc gac gtg gtg ttc ctg tgc gtg 307  
Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val Val Phe Leu Cys Val  
55 60 65

aag ccg aaa ttt atc gtc gaa gtg ctc tcc gaa atc acc ggc act ttg 355  
Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu Ile Thr Gly Thr Leu  
70 75 80 85

gat aac aac tcc gca caa agt gtt gtg gtc agc atg gcc gca ggc atc 403  
Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser Met Ala Ala Gly Ile  
90 95 100

agc atc gct gcc atg gaa gaa agc gcc tct gcg ggg ctc ccc gtc gtg 451  
 Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala Gly Leu Pro Val Val  
 105 110 115

cgc gtc atg ccg aac act cca atg ctc gtg ggc aag ggc atg tgc act 499  
 Arg Val Met Pro Asn Thr Pro Met Leu Val Gly Lys Gly Met Ser Thr  
 120 125 130

gtc acc aaa ggc cgc tac gtt gac gcg gaa cag ttg gaa caa gtc aag 547  
Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln Leu Glu Gln Val Lys  
135 140 145

gac ttg ttg agc acc gtt gga gac gtc ctc gaa gtc gcg gaa tca gac 595  
Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu Val Ala Glu Ser Asp  
150 155 160 165

atc gac gca gtc acc gcg atg tcc gga tcc tcc cct gca tac ctg ttc 643

Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser Pro Ala Tyr Leu Phe  
 170 175 180  
 ctt gtg acc gaa gcg ctc att gag gca gga gtt aat cta ggc ctg ccc 691  
 Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val Asn Leu Gly Leu Pro  
 185 190 195  
 cgc gcg acc gct aaa aag ctc gct gtg gcc tca ttc gaa ggt gct gca 739  
 Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser Phe Glu Gly Ala Ala  
 200 205 210  
 acc atg atg aag gaa acc ggc aaa gaa ccc tca gaa ttg cgc gca ggc 787  
 Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser Glu Leu Arg Ala Gly  
 215 220 225  
 gtt tcc tca ccc gca ggc acc acc gtc gca gcc atc cga gaa ctc gaa 835  
 Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala Ile Arg Glu Leu Glu  
 230 235 240 245  
 gaa agc gga atc cga ggc gct ttc tac cgc gca gcc caa gct tgc gcc 883  
 Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala Ala Gln Ala Cys Ala  
 250 255 260  
 gac cga tct gaa gaa ctc gga aag cgc tagaaaccgt tatttccccg 930  
 Asp Arg Ser Glu Glu Leu Gly Lys Arg  
 265 270  
 tta 933  
  
 <210> 298  
 <211> 270  
 <212> PRT  
 <213> Corynebacterium glutamicum  
  
 <400> 298  
 Met Thr Thr Ile Ala Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu  
 1 5 10 15  
 Val Ser Gly Leu Ile Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val  
 20 25 30  
 Thr Asn Arg Ser Glu Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly  
 35 40 45  
 Ile Leu Asn Met Thr Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val  
 50 55 60  
 Val Phe Leu Cys Val Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu  
 65 70 75 80  
 Ile Thr Gly Thr Leu Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser  
 85 90 95  
 Met Ala Ala Gly Ile Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala  
 100 105 110  
 Gly Leu Pro Val Val Arg Val Met Pro Asn Thr Pro Met Leu Val Gly  
 115 120 125  
 Lys Gly Met Ser Thr Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln

130	135	140
Leu Glu Gln Val Lys Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu 145 150 155 160		
Val Ala Glu Ser Asp Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser 165 170 175		
Pro Ala Tyr Leu Phe Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val 180 185 190		
Asn Leu Gly Leu Pro Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser 195 200 205		
Phe Glu Gly Ala Ala Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser 210 215 220		
Glu Leu Arg Ala Gly Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala 225 230 235 240		
Ile Arg Glu Leu Glu Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala 245 250 255		
Ala Gln Ala Cys Ala Asp Arg Ser Glu Glu Leu Gly Lys Arg 260 265 270		

<210> 299  
 <211> 1296  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1273)  
 <223> RXS02157

<400> 299  
 ggggtggaatt ggcacgatgg tgctgccgga tgtttttgat cgggagaatt atcctgaagg 60  
 caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115  
 Met Ser Thr Leu Glu  
 1 5  
 act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163  
 Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu  
 10 15 20  
 ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211  
 Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val  
 25 30 35  
 tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259  
 Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala  
 40 45 50  
 cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307  
 His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly  
 55 60 65  
 cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355



His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu	
70 75 80 85	
gag ctc atc aag cgt ttt tgc ctt gac gac gcc acc ctc gcc gcg caa	403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln	
90 95 100	
acc cgg gtt ttc ttc tgc aac tgc ggc gcc gaa gca aac gag gct gct	451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala	
105 110 115	
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt	499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val	
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cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag	547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln	
135 140 145	
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc	595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe	
150 155 160 165	
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Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn	
170 175 180	
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg	691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr	
185 190 195	
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg	739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu	
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Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly	
215 220 225	
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt	835
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val	
230 235 240 245	
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc	883
Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile	
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ggc gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc	931
Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly	
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Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala	
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Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala	
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cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt  
1075

Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
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gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc  
1123

Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
330 335 340

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1171

Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
345 350 355

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1219

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360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca  
1267

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1296

Ile Ala

390

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Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
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Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
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Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
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Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
100 105 110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg  
115 120 125

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 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys  
 165 170 175  
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 195 200 205  
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp  
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 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln  
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 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly  
 245 250 255  
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu  
 260 265 270  
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 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala  
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 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly  
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 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe  
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 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu  
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Met Thr Ala Thr Tyr  
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Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met  
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Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu  
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aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307  
Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu  
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Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr  
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Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His  
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Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val  
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Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val  
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170 175 180  
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc 691  
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly  
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Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile  
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 gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca 835  
 Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro  
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 Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro  
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 gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc 931  
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 265 270 275  
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 295 300 305  
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 Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala  
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 Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly  
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 Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr  
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 180 185 190  
 Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys  
 195 200 205  
 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val  
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 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly  
 225 230 235 240  
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala  
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 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys  
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<223> RXS02970

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 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
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cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
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gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
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 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
 70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
 90 95 100

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 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
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tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
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tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr 170 175 180			643
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser 185 190 195			691
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys 200 205 210			739
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala 215 220 225			787
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gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile 250 255 260			883
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ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys 330 335 340			
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala 345 350 355			
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Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
375          380          385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390          395          400          405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
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Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
410          415          420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
1411
Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
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1459
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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35          40          45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50          55          60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
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His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
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Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
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Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe

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His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg 165 170 175		
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro 180 185 190		
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys 195 200 205		
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Leu Ala Leu Lys Gly  
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Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
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His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
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Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
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Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
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Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
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Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
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230 235 240 245	
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Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	
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Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	
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Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
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1123	
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
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1171	
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	
1219	
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
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gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	
1267	
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	

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 gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
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 Phe Lys Glu Arg Gly  
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 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
                     35                      40                      45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
   50                      55                      60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
   65                      70                      75                      80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
                     85                      90                      95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
                     100                      105                      110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
                     115                      120                      125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
   130                      135                      140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
   145                      150                      155                      160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
                     165                      170                      175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
                     180                      185                      190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
                     195                      200                      205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
   210                      215                      220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
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 Met Thr Ser Met Asn  
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 ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163  
 Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val  
 10 15 20  
 cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat 211  
 Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp  
 25 30 35

gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gag gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcc atc	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile	
170 175 180	
aag gtc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag gcc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Ala	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883
Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
250 255 260	
ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc	931
Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg	
265 270 275	

gag cgc gtc aac aca ggc ggg gcg ggc gtt aag gtt cgc ctg gtc aag 979  
 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys  
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ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc ggc tgg  
 1027  
 Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp  
 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag  
 1075  
 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys  
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc  
 1123  
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg  
 330 335 340

ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg  
 1171  
 Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu  
 345 350 355

ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg  
 1219  
 Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu  
 360 365 370

cag ggc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt  
 1267  
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly  
 375 380 385

gag ctg ctg ctt tac gta cca gcc gtg cgc cca caa gaa ttc gac gtg  
 1315  
 Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val  
 390 395 400 405

gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa  
 1363  
 Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu Asn Ala Ala Ser Glu  
 410 415 420

aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc  
 1411  
 Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe  
 425 430 435

aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg  
 1459  
 Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr  
 440 445 450

ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc  
 1507  
 Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser  
 455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc  
 1555



Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro  
 470 475 480 485  
 gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc  
 1603  
 Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala  
 490 495 500  
 gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg  
 1651  
 Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro  
 505 510 515  
 gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc  
 1699  
 Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg  
 520 525 530  
 gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag  
 1747  
 Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu  
 535 540 545  
 att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg  
 1795  
 Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu  
 550 555 560 565  
 atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac  
 1843  
 Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp  
 570 575 580  
 ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg  
 1891  
 Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu  
 585 590 595  
 gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc  
 1939  
 Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg  
 600 605 610  
 gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct  
 1987  
 Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala  
 615 620 625  
 gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa  
 2035  
 Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys  
 630 635 640 645  
 ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc  
 2083  
 Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu  
 650 655 660  
 tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct  
 2131  
 Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala

665					670					675				
aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc														
2179														
Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His	Glu	His	Val	Asp
			680				685					690		
gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg														
2227														
Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala	Met	Phe	Ser	Ser
		695				700					705			Trp
cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc														
2275														
Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser	Gly	Lys	Asn	Ala
						715					720			725
gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg														
2323														
Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala	Val	Ala	Asp	Leu
				730					735					740
aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc														
2371														
Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys	Ser	Ala	Ala	Ser
			745				750						755	Leu
ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag														
2419														
Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu	Arg	Phe	Arg	Lys
		760					765					770		Gln
ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc														
2467														
Leu	Val	Asp	Ala	Ala	Ser	Ser	Leu	Ile	Val	Asp	Trp	Pro	Thr	Asn
		775				780					785			Pro
tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac														
2515														
Ser	Ala	Thr	Val	Gly	Pro	Leu	Thr	Glu	Leu	Pro	Ser	Asp	Lys	Leu
						795					800			805
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc														
2563														
His	Ala	Leu	Thr	Thr	Leu	Glu	Glu	Gly	Glu	Ser	Trp	Leu	Leu	Lys
				810					815					820
cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa														
2611														
Arg	Gln	Leu	Asp	Asp	Thr	Gly	Arg	Leu	Trp	Ser	Pro	Gly	Ile	Lys
			825					830					835	Glu
ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca														
2659														
Gly	Val	Lys	Pro	Gly	Thr	Phe	Phe	His	Leu	Thr	Glu	Val	Phe	Gly
		840					845					850		Pro
gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc														
2707														
Val	Leu	Gly	Leu	Met	Lys	Ala	Thr	Asp	Leu	Asn	Glu	Ala	Ile	Glu
		855				860					865			Phe

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac  
2755

Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp  
870 875 880 885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc  
2803

Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala  
890 895 900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc  
2851

Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe  
905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga  
2899

Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly  
920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac  
2947

Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His  
935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc  
2995

His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro  
950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca  
3043

Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr  
970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat  
3091

Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp  
985 990 995

gta gaa gcc aac att ttc cgc tac cga cca gca gag gta gta ctc cga  
3139

Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala Glu Val Val Leu Arg  
1000 1005 1010

ctc gac gat tcc gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca  
3187

Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala  
1015 1020 1025

gcc cgt cgc gcc ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt  
3235

Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val  
1030 1035 1040 1045

tca gag caa gtc cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa  
3283

Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu  
1050 1055 1060

aca gtc gat gat tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac  
3331

Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr  
1065 1070 1075

gac gag aac tcc agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac  
3379

Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp  
1080 1085 1090

act gtc cgt gaa cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac  
3427

Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp  
1095 1100 1105

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3475

Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys  
1110 1115 1120 1125

gaa caa gca att tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg  
3523

Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala  
1130 1135 1140

gcc ttc cac gag ttg gcg gag gaa ctt aaa cgt tgatcggtttt gcgcattgggt  
3576

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3579

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35 40 45

Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr  
50 55 60

Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile  
65 70 75 80

Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly  
85 90 95

Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg  
100 105 110

Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp  
 115 120 125  
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg  
 130 135 140  
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala  
 145 150 155 160  
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val  
 165 170 175  
 Glu Tyr Val Ser Ile Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met  
 180 185 190  
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro  
 195 200 205  
 Leu Tyr Ile Glu Ala Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn  
 210 215 220  
 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe  
 225 230 235 240  
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile  
 245 250 255  
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu  
 260 265 270  
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys  
 275 280 285  
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala  
 290 295 300  
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr  
 305 310 315 320  
 Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn  
 325 330 335  
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile  
 340 345 350  
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val  
 355 360 365  
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val  
 370 375 380  
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro  
 385 390 395 400  
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu  
 405 410 415  
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala  
 420 425 430  
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile

435					440					445					
Ser	Asp	Leu	Ala	Thr	Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His
450					455					460					
Thr	Gln	Asp	Arg	Ser	Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro
465					470					475					480
Phe	Ile	Asn	Glu	Pro	Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln
				485					490					495	
Trp	Ala	Thr	Lys	Ala	Val	Ala	Thr	Ala	Ala	Glu	Pro	Gly	Trp	Leu	Glu
			500					505					510		
Lys	Gln	Thr	Lys	Pro	Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu
		515					520					525			
Ile	Asn	Asp	Val	Arg	Asp	Ala	Ala	Glu	Ala	Trp	Ala	Ala	Arg	Pro	Ala
		530				535					540				
Arg	Glu	Arg	Ala	Glu	Ile	Leu	Tyr	Lys	Thr	Ala	Glu	Ile	Leu	Arg	Val
545					550					555					560
Arg	Arg	Gly	His	Leu	Ile	Ser	Val	Thr	Ala	Ala	Glu	Val	Gly	Lys	Ala
				565					570					575	
Val	Glu	Gln	Thr	Asp	Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg
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Phe	Thr	Pro	Asp	Arg	Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro
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Ile	Ala	Ile	Pro	Ala	Gly	Ser	Thr	Phe	Ala	Ala	Leu	Ala	Ala	Gly	Ala
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Gly	Val	Ile	His	Lys	Pro	Ser	Lys	Pro	Ser	Gln	His	Cys	Ser	Ala	Ala
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Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His
		675					680					685			
Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala
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Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala
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Ser	Ala	Ala	Ser	Leu	Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu
		755					760					765			

Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp  
 770 775 780  
 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro  
 785 790 795 800  
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser  
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 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser  
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 Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr  
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 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly  
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 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val  
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 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val  
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 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly  
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 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala  
 930 935 940  
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 945 950 955 960  
 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn  
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 980 985 990  
 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala  
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Gly Lys Val Ser Asp Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu  
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Val Val Leu Leu Asp Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu  
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Arg Tyr Trp Leu Lys Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe  
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<223> FRXA00023

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 Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala  
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 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val  
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 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp  
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tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac gac gag aac tcc 240  
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser  
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agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac act gtc cgt gaa 288  
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu  
 85 90 95

cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac gat gca gta act 336  
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr  
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gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa gaa caa gca att 384  
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile  
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 Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu



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 50 55 60  
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser  
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 85 90 95  
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr  
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 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile  
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 Met Thr Ser Met Asn  
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ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg	163
Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val	
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cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat	211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
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gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
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Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
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Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
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Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
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Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
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Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gaa gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
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Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa	
170 175 180	
nnn ntc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag ccc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
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Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883

Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile	Val	Leu	Gln	Ala	Tyr		
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ctt	ccc	gat	gcc	ctc	ggg	gca	atc	cag	gac	ttg	gcg	cag	ttc	ggc	cgc	931	
Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu	Ala	Gln	Phe	Gly	Arg		
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gag	cgc	gtc	aac	aca	ggc	ggg	gcg	ggc	gtt	aag	gtt	cgc	ctg	gtc	aag	979	
Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys	Val	Arg	Leu	Val	Lys		
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ggg	gct	aat	ttg	cct	atg	gag	cac	gtc	cac	gcg	cag	atc	acc	ggc	tgg		
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cca	gtt	gcc	aca	gaa	cct	tcc	aaa	caa	gcc	acc	gat	gcc	aat	tac	aag		
1075																	
Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr	Asp	Ala	Asn	Tyr	Lys		
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cgc	gtc	ctc	tat	tgg	acg	atg	cgc	aaa	gaa	aac	atg	gag	ggc	ctg	cgc		
1123																	
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ctg	ggc	gtt	gcc	ggc	cac	aac	ctt	ttc	gac	ata	gca	ttc	gca	cat	ttg		
1171																	
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1219																	
Leu	Ser	Val	Glu	Arg	Gly	Val	Ala	Asp	Arg	Val	Glu	Phe	Glu	Met	Leu		
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cag	ggc	atg	gcg	tcc	gat	cag	gcg	cgc	gcc	gtc	agc	gtt	gac	gtc	ggg		
1267																	
Gln	Gly	Met	Ala	Ser	Asp	Gln	Ala	Arg	Ala	Val	Ser	Val	Asp	Val	Gly		
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gag	ctg	ctg	ctt	tac	gta	cca	gcc	gtg	cgc	cca	caa	gaa	ttc	gac	gtg		
1315																	
Glu	Leu	Leu	Leu	Tyr	Val	Pro	Ala	Val	Arg	Pro	Gln	Glu	Phe	Asp	Val		
390					395					400					405		
gcc	att	tct	tac	ctc	gtg	cgc	cgc	ctc	gag	gaa	aac	gcc	gcg	agc	gaa		
1363																	
Ala	Ile	Ser	Tyr	Leu	Val	Arg	Arg	Leu	Glu	Glu	Asn	Ala	Ala	Ser	Glu		
				410					415					420			
aac	ttc	atg	tcc	gcc	atc	ttc	gac	ctc	gac	gcc	gac	aac	ccg	tcc	ttc		
1411																	
Asn	Phe	Met	Ser	Ala	Ile	Phe	Asp	Leu	Asp	Ala	Asp	Asn	Pro	Ser	Phe		
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aag	cga	gag	gag	agc	cgc	ttc	cgc	gcc	tcc	ata	tct	gac	ctc	gcc	acg		
1459																	
Lys	Arg	Glu	Glu	Ser	Arg	Phe	Arg	Ala	Ser	Ile	Ser	Asp	Leu	Ala	Thr		
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ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc  
1507

Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser  
455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc  
1555

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro  
470 475 480 485

gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc  
1603

Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala  
490 495 500

gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg  
1651

Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro  
505 510 515

gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc  
1699

Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg  
520 525 530

gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag  
1747

Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu  
535 540 545

att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg  
1795

Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu  
550 555 560 565

atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac  
1843

Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp  
570 575 580

ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg  
1891

Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu  
585 590 595

gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc  
1939

Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg  
600 605 610

gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct  
1987

Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala  
615 620 625

gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa  
2035

Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys  
630 635 640 645

ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc  
2083

Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu  
650 655 660

tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct  
2131

Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala  
665 670 675

aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc  
2179

Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg  
680 685 690

gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg  
2227

Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp  
695 700 705

cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc  
2275

Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile  
710 715 720 725

gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg  
2323

Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val  
730 735 740

aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc  
2371

Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu  
745 750 755

ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag  
2419

Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln  
760 765 770

ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc  
2467

Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro  
775 780 785

tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac  
2515

Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His  
790 795 800 805

cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc  
2563

His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro  
810 815 820

cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa  
2611

Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu  
825 830 835

ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca  
 2659  
 Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro  
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 Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe  
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 Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe  
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 2899  
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 2947  
 Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His  
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cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc  
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 His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro  
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 Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr  
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<213> Corynebacterium glutamicum

&lt;400&gt; 312

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Lys	Gln	Phe	Ala	Lys	Ala	Val	Ala	Glu	Ile	Gln	Ser	Asp	Gly	His	Arg
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Ala	Lys	His	Leu	Asp	Asp	Thr	Val	Arg	Leu	Leu	Arg	Arg	Pro	Asp	Val
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Glu	Tyr	Val	Ser	Xaa	Xaa	Xaa	Ser	Ser	Val	Ala	Ser	Gln	Ile	Ser	Met
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225					230					235					240
Lys	Arg	Leu	Leu	Ser	Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile
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Val	Leu	Gln	Ala	Tyr	Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu
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Ala	Gln	Phe	Gly	Arg	Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys
		275					280					285			
Val	Arg	Leu	Val	Lys	Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala
	290					295					300				
Gln	Ile	Thr	Gly	Trp	Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr
305					310					315					320

Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn  
 325 330 335  
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile  
 340 345 350  
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val  
 355 360 365  
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val  
 370 375 380  
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro  
 385 390 395 400  
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu  
 405 410 415  
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala  
 420 425 430  
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile  
 435 440 445  
 Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His  
 450 455 460  
 Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro  
 465 470 475 480  
 Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln  
 485 490 495  
 Trp Ala Thr Lys Ala Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu  
 500 505 510  
 Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu  
 515 520 525  
 Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala  
 530 535 540  
 Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val  
 545 550 555 560  
 Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala  
 565 570 575  
 Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg  
 580 585 590  
 Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu  
 595 600 605  
 Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro  
 610 615 620  
 Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala  
 625 630 635 640  
 Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala



645							650							655						
Val	Val	Glu	Ala	Leu	Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His					
			660					665						670						
Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His					
		675					680					685								
Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala					
	690					695					700									
Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser					
705					710					715					720					
Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala					
				725					730					735						
Val	Ala	Asp	Leu	Val	Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys					
			740					745					750							
Ser	Ala	Ala	Ser	Leu	Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu					
		755					760					765								
Arg	Phe	Arg	Lys	Gln	Leu	Val	Asp	Ala	Ala	Ser	Ser	Leu	Ile	Val	Asp					
	770					775					780									
Trp	Pro	Thr	Asn	Pro	Ser	Ala	Thr	Val	Gly	Pro	Leu	Thr	Glu	Leu	Pro					
785					790					795					800					
Ser	Asp	Lys	Leu	His	His	Ala	Leu	Thr	Thr	Leu	Glu	Glu	Gly	Glu	Ser					
				805					810					815						
Trp	Leu	Leu	Lys	Pro	Arg	Gln	Leu	Asp	Asp	Thr	Gly	Arg	Leu	Trp	Ser					
			820					825					830							
Pro	Gly	Ile	Lys	Glu	Gly	Val	Lys	Pro	Gly	Thr	Phe	Phe	His	Leu	Thr					
		835					840					845								
Glu	Val	Phe	Gly	Pro	Val	Leu	Gly	Leu	Met	Lys	Ala	Thr	Asp	Leu	Asn					
	850					855					860									
Glu	Ala	Ile	Glu	Phe	Gln	Asn	Gly	Asn	Asp	Phe	Gly	Leu	Thr	Gly	Gly					
865					870					875					880					
Leu	Gln	Ser	Leu	Asp	Ala	Asp	Glu	Val	Arg	Thr	Trp	Leu	Asp	His	Val					
				885					890					895						
Asp	Val	Gly	Asn	Ala	Tyr	Val	Asn	Arg	Gly	Ile	Thr	Gly	Ala	Ile	Val					
			900					905					910							
Gln	Arg	Gln	Ser	Phe	Gly	Gly	Trp	Lys	Lys	Ser	Ser	Val	Gly	Leu	Gly					
		915					920					925								
Ser	Lys	Ala	Gly	Gly	Pro	Asn	Tyr	Val	Met	Leu	Met	Gly	Thr	Trp	Ala					
	930					935					940									
Asp	Ala	Pro	Ser	His	His	Ala	Pro	Arg	Glu	Thr	Asn	Pro	Leu	Ile	Ser					
945					950															

Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp  
 980 985 990

Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala  
 995 1000 1005

<210> 313

<211> 927

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(904)

<223> RXC02498

<400> 313

caaggtagaa atttgtccgt gggcacttcg tgaaggtgtg atcctcacca ggatcgacaa 60

aggactcgag taacatttac ccggaaagga gttggcgaaa atg agt gaa gag aaa 115  
 Met Ser Glu Glu Lys  
 1 5

ctc aca gtc gct gag ctg atg gcg cgt gcc gcg aaa gag gga cgc tcc 163  
 Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser  
 10 15 20

acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc 211  
 Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly  
 25 30 35

gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag 259  
 Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys  
 40 45 50

ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa 307  
 Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu  
 55 60 65

cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa 355  
 Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu  
 70 75 80 85

gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt 403  
 Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg  
 90 95 100

ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa 451  
 Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu  
 105 110 115

aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca 499  
 Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala  
 120 125 130

gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat 547

Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp  
 135 140 145

gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac 595  
 Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn  
 150 155 160 165

act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca 643  
 Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro  
 170 175 180

gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc 691  
 Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile  
 185 190 195

gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg 739  
 Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu  
 200 205 210

tgg gag cgc ctg aac aag tgg atc gtc gct gtt ctg gca gtc ggc gtg 787  
 Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val  
 215 220 225

acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat 835  
 Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp  
 230 235 240 245

ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc 883  
 Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe  
 250 255 260

ggg ccg ctg gca atc gtc atg taatttgtcg ttttgggccc ccg 927  
 Gly Pro Leu Ala Ile Val Met  
 265

&lt;210&gt; 314

&lt;211&gt; 268

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 314

Met Ser Glu Glu Lys Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala  
 1 5 10 15

Lys Glu Gly Arg Ser Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser  
 20 25 30

Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro  
 35 40 45

Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile  
 50 55 60

Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro  
 65 70 75 80

Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln  
 85 90 95

Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu

100	105	110
Arg Ile Val Asp Glu Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe 115 120 125		
Pro Val Val Pro Ala Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala 130 135 140		
Glu Lys Asp Ala Asp Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu 145 150 155 160		
Val Glu Val Asp Asn Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu 165 170 175		
Val Asp Glu Glu Pro Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile 180 185 190		
Ile Met Met Ala Ile Val Gly Val Val Leu Gly Val Val Val Phe Leu 195 200 205		
Gly Phe Glu Met Leu Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val 210 215 220		
Leu Ala Val Gly Val Thr Leu Gly Met Val Gly Ile Ile His Ala Leu 225 230 235 240		
Arg Thr Ser Arg Asp Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly 245 250 255		
Leu Val Met Thr Phe Gly Pro Leu Ala Ile Val Met 260 265		

&lt;210&gt; 315

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(751)

&lt;223&gt; RXA01491

&lt;400&gt; 315

aacggtgtga aacacattga agtgtcgttg gggtatccgc gcgaatggga gcattggtct 60

gggcagcatg tgtggccata tccagtgatg gaggtggaca atg ctg gat gag tct	115
Met Leu Asp Glu Ser	
1 5	

ttg ttt cca aat tcg gca aag ttt tct ttc att aaa act ggc gat gct	163
Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile Lys Thr Gly Asp Ala	
10 15 20	

gtt aat tta gac cat ttc cat cag ttg cat ccg ttg gaa aag gca ctg	211
Val Asn Leu Asp His Phe His Gln Leu His Pro Leu Glu Lys Ala Leu	
25 30 35	

gta gcg cac tcg gtt gat att aga aaa gca gag ttt gga gat gcc agg	259
Val Ala His Ser Val Asp Ile Arg Lys Ala Glu Phe Gly Asp Ala Arg	
40 45 50	

tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat 307  
 Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp  
 55 60 65  
 ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355  
 Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val  
 70 75 80 85  
 tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg 403  
 Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala  
 90 95 100  
 cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451  
 Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu  
 105 110 115  
 ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499  
 Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile  
 120 125 130  
 cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547  
 Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg  
 135 140 145  
 ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595  
 Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu  
 150 155 160 165  
 acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat 643  
 Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp  
 170 175 180  
 gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691  
 Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro  
 185 190 195  
 ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg 739  
 Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala  
 200 205 210  
 act gca gtg act tgaactggat ggagaggata cct 774  
 Thr Ala Val Thr  
 215

&lt;210&gt; 316

&lt;211&gt; 217

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 316

Met Leu Asp Glu Ser Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile  
 1 5 10 15  
 Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro  
 20 25 30  
 Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu  
 35 40 45

Phe Gly Asp Ala Arg Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly  
 50 55 60  
 Arg Asp Ser Gly Asp Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu  
 65 70 75 80  
 Trp Pro Ser Ser Val Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg  
 85 90 95  
 Ala Ala Val Val Ala Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp  
 100 105 110  
 Ala Glu Pro Ala Glu Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala  
 115 120 125  
 Arg Val Gly Glu Ile Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val  
 130 135 140  
 His Cys Ala Asp Arg Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys  
 145 150 155 160  
 Ala Trp Phe Pro Leu Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu  
 165 170 175  
 Ile Asp Leu Arg Asp Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg  
 180 185 190  
 Pro Thr Pro Val Pro Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly  
 195 200 205  
 Tyr Val Ile Ala Ala Thr Ala Val Thr  
 210 215

&lt;210&gt; 317

&lt;211&gt; 1287

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1264)

&lt;223&gt; RXA02155

&lt;400&gt; 317

tcggcgctgc accttaaagt agcgccttaa agcggcgctt caaaccaagc gccctaacca 60

gcaaacacaa caaacacatc taattcagta ggagttccac atg gca gaa aaa ggc 115  
 Met Ala Glu Lys Gly  
 1 5

att acc gcg ccg aaa ggc ttc gtt gct tct gca acg acc gcg ggt att 163  
 Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala Thr Thr Ala Gly Ile  
 10 15 20

aaa gct tct ggc aat cct gac atg gcg ttg gtg gtt aac cag ggt cca 211  
 Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val Val Asn Gln Gly Pro  
 25 30 35

gag ttt tcc gca gcg gcc gtg ttt aca cgt aac cga gtt ttc gca gcg 259  
 Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn Arg Val Phe Ala Ala

40	45	50	
cct gtg aag gtg agc cga gag aac gtt gct gat ggc cag atc agg gct Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp Gly Gln Ile Arg Ala 55 60 65			307
gtt ttg tac aac gct ggt aat gct aat gcg tgt aat ggt ctg cag ggt Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys Asn Gly Leu Gln Gly 70 75 80 85			355
gag aag gat gct cgt gag tct gtt tct cat cta gct caa aat ttg ggc Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu Ala Gln Asn Leu Gly 90 95 100			403
ttg gag gat tcc gat att ggt gtg tgt tcc act ggt ctt att ggt gag Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr Gly Leu Ile Gly Glu 105 110 115			451
ttg ctt ccg atg gat aag ctc aat gca ggt att gat cag ctg acc gct Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile Asp Gln Leu Thr Ala 120 125 130			499
gag ggc gct ttg ggt gac aat ggt gca gct gct gcc aag gcg atc atg Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala Ala Lys Ala Ile Met 135 140 145			547
acc act gac acg gtg gat aag gaa acc gtc gtg ttt gct gat ggt tgg Thr Thr Asp Thr Val Lys Glu Thr Val Phe Ala Asp Gly Trp 150 155 160 165			595
act gtc ggc gga atg ggc aag ggc gtg ggc atg atg gcg ccg tct ctt Thr Val Gly Gly Met Gly Lys Gly Val Gly Met Met Ala Pro Ser Leu 170 175 180			643
gcc acc atg ctg gtc tgc ttg acc act gat gca tcc gtt act cag gaa Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala Ser Val Thr Gln Glu 185 190 195			691
atg gct cag atc gcg ctg gct aat gct acg gcc gtt acg ttt gac acc Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala Val Thr Phe Asp Thr 200 205 210			739
ctg gat att gat gga tca acc tcc acc aat gac acc gtg ttc ctg ctg Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp Thr Val Phe Leu Leu 215 220 225			787
gca tct ggc gct agc gga atc acc cca act cag gat gaa ctc aac gat Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln Asp Glu Leu Asn Asp 230 235 240 245			835
gcg gtg tac gca gct tgt tct gat atc gca gcg aag ctt cag gct gat Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala Lys Leu Gln Ala Asp 250 255 260			883
gca gag ggt gtg acc aag cgc gtt gct gtg aca gtg gtg gga acc acc Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr Val Val Gly Thr Thr 265 270 275			931
aac aac gag cag gcg att aat gcg gct cgc act gtt gct cgt gac aat Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr Val Ala Arg Asp Asn 280 285 290			979

ttg ttc aag tgc gca atg ttt gga tct gat cca aac tgg ggt cgc gtg  
1027

Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro Asn Trp Gly Arg Val  
295 300 305

ttg gct gca gtc ggc atg gct gat gct gat atg gaa cca gag aag att  
1075

Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met Glu Pro Glu Lys Ile  
310 315 320 325

tct gtg ttc ttc aat ggt caa gca gta tgc ctt gat tcc act ggc gct  
1123

Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala  
330 335 340

cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga  
1171

Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg  
345 350 355

att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act  
1219

Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr  
360 365 370

gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct  
1264

Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser Ala Tyr Ser Ser  
375 380 385

taaaaagaaa cagcactcca act  
1287

<210> 318

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met Ala Glu Lys Gly Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala  
1 5 10 15

Thr Thr Ala Gly Ile Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val  
20 25 30

Val Asn Gln Gly Pro Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn  
35 40 45

Arg Val Phe Ala Ala Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp  
50 55 60

Gly Gln Ile Arg Ala Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys  
65 70 75 80

Asn Gly Leu Gln Gly Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu  
85 90 95

Ala Gln Asn Leu Gly Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr  
100 105 110



Gly Leu Ile Gly Glu Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile  
 115 120 125  
 Asp Gln Leu Thr Ala Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala  
 130 135 140  
 Ala Lys Ala Ile Met Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val  
 145 150 155 160  
 Phe Ala Asp Gly Trp Thr Val Gly Gly Met Gly Lys Gly Val Gly Met  
 165 170 175  
 Met Ala Pro Ser Leu Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala  
 180 185 190  
 Ser Val Thr Gln Glu Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala  
 195 200 205  
 Val Thr Phe Asp Thr Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp  
 210 215 220  
 Thr Val Phe Leu Leu Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln  
 225 230 235 240  
 Asp Glu Leu Asn Asp Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala  
 245 250 255  
 Lys Leu Gln Ala Asp Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr  
 260 265 270  
 Val Val Gly Thr Thr Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr  
 275 280 285  
 Val Ala Arg Asp Asn Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro  
 290 295 300  
 Asn Trp Gly Arg Val Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met  
 305 310 315 320  
 Glu Pro Glu Lys Ile Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu  
 325 330 335  
 Asp Ser Thr Gly Ala Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala  
 340 345 350  
 Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala  
 355 360 365  
 Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser  
 370 375 380  
 Ala Tyr Ser Ser  
 385

&lt;210&gt; 319

&lt;211&gt; 1074

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1051)

&lt;223&gt; RXA02156

&lt;400&gt; 319

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aaccactgac ctgagcttct cctacgtgga gatcaactcc gcgtacagct cttaaaaaga 60

aacagcactc caactaacaa gcagggaaaa gggcacaggc atg aat gac ttg atc 115
                                         Met Asn Asp Leu Ile
                                           1           5

aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163
Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu
                        10                        15                        20

cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211
Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly
                        25                        30                        35

gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259
Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp
                        40                        45                        50

atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307
Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly
                        55                        60                        65

ggg gga cct cag att tct gag atg cta aac cgt gtg ggt ctc cag ggc 355
Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly
                        70                        75                        80                        85

gag ttc aag ggt ggt ttc cgt gtg acc act cct gag gtc atg gac att 403
Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile
                        90                        95                        100

gtg cgc atg gtg ctc ttt ggt cag gtc ggt cgc gat tta gtt ggt ttg 451
Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu
                        105                        110                        115

atc aac tct cat ggc cct tac gct gtg gga acc tcc ggt gag gat gcc 499
Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala
                        120                        125                        130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547
Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn Ile Asp Gly Val Pro
                        135                        140                        145

act gat att ggt ttg gtc gga gac atc att aat gtc gat gcc tct tcc 595
Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser
                        150                        155                        160                        165

ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643
Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile
                        170                        175                        180

gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691
Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala
                        185                        190                        195

gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739

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Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu  
 200 205 210

acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787  
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu  
 215 220 225

gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835  
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu  
 230 235 240 245

gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883  
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg  
 250 255 260

ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931  
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser  
 265 270 275

gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979  
 Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu  
 280 285 290

ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga  
 1027  
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg  
 295 300 305

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 1074  
 Lys Asp Asp Lys Asp Gly Glu Leu  
 310 315

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 <211> 317  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 320  
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Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val  
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Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala  
 35 40 45

Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro  
 50 55 60

Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg  
 65 70 75 80

Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro  
 85 90 95

Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg  
 100 105 110

Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr  
 115 120 125  
 Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn  
 130 135 140  
 Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn  
 145 150 155 160  
 Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro  
 165 170 175  
 Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile  
 180 185 190  
 Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu  
 195 200 205  
 Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro  
 210 215 220  
 Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala  
 225 230 235 240  
 Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys  
 245 250 255  
 Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly  
 260 265 270  
 Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile  
 275 280 285  
 Gly Thr Met Val Leu Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu  
 290 295 300  
 Gly Thr Val Phe Arg Lys Asp Asp Lys Asp Gly Glu Leu  
 305 310 315

&lt;210&gt; 321

&lt;211&gt; 903

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(880)

&lt;223&gt; RXN02153

&lt;400&gt; 321

cccacttgca gtttagctg taggtgggtt tttgcatgtc taaccgtct tttatgcaca 60

cccccgcaat gaatcaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115  
 Met Ile Met His Asn  
 1 5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163  
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser  
 10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct	211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala	
25 30 35	
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc	259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr	
40 45 50	
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg	307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala	
55 60 65	
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat	355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp	
70 75 80 85	
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt	403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu	
90 95 100	
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt	451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg	
105 110 115	
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag	499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln	
120 125 130	
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct	547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala	
135 140 145	
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt	595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly	
150 155 160 165	
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca	643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro	
170 175 180	
gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa	691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys	
185 190 195	
gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg	739
Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala	
200 205 210	
tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac	787
Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn	
215 220 225	
ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg	835
Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val	
230 235 240 245	
ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt	880
Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu	
250 255 260	
tgaaagaagg cgttaccgca gaa	903

&lt;210&gt; 322

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 322

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Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala
 1             5             10             15

Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu
      20             25             30

Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
      35             40             45

Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
      50             55             60

Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
      65             70             75             80

Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
      85             90             95

Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys
      100            105            110

Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
      115            120            125

Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
      130            135            140

Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly
      145            150            155            160

Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala
      165            170            175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
      180            185            190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
      195            200            205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
      210            215            220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
      225            230            235            240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
      245            250            255

Gln Pro His Leu
      260

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&lt;210&gt; 323

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<211> 903
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (880)  
<223> FRXA02153
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<400> 323																
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cccccgcaat gaatcaaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115																
Met Ile Met His Asn 5																
1																
gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163																
Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser 20																
10 15																
gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211																
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala 35																
25 30																
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259																
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr 50																
40 45																
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307																
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala 65																
55 60																
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355																
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp 85																
70 75 80																
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403																
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu 100																
90 95																
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451																
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg 115																
105 110																
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499																
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln 130																
120 125																
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct 547																
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala 145																
135 140																
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595																
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly 165																
150 155 160																
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643																
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro 180																
170 175																
gat gtt tcc gta gtg tcc atc acc gcc gta tca ggt gca ggt aag aaa 691																

Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys  
 185 190 195  
 gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739  
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala  
 200 205 210  
 tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787  
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn  
 215 220 225  
 ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835  
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val  
 230 235 240 245  
 ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880  
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 tgaaagaagg cgttaccgca gaa 903

<210> 324  
 <211> 260  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 324  
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 Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu  
 35 40 45  
 Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His  
 50 55 60  
 Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr  
 65 70 75 80  
 Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser  
 85 90 95  
 Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys  
 100 105 110  
 Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr  
 115 120 125  
 Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro  
 130 135 140  
 Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly  
 145 150 155 160  
 Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala  
 165 170 175



Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser  
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met  
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro  
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val  
 225 230 235 240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu  
 245 250 255

Gln Pro His Leu  
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<210> 325  
 <211> 414  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(391)  
 <223> RXA02154

<400> 325  
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caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115  
 Leu Lys Glu Gly Val  
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163  
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu  
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211  
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala  
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259  
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu  
 40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307  
 Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly  
 55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355  
 Thr Ala Gly Ala Ala Gln Cys Met Asn Leu Ser Val Gly Phe Asp  
 70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401  
 Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro  
 90 95

ccttaaagcg gcg 414



55	60	65	
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu 70 75 80 85			355
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln 90 95 100			403
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala 105 110 115			451
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val 120 125 130			499
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln 135 140 145			547
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe 150 155 160 165			595
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn 170 175 180			643
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr 185 190 195			691
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu 200 205 210			739
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly 215 220 225			787
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val 230 235 240 245			835
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile 250 255 260			883
ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly 265 270 275			931
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala 280 285 290			979
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala			

295 300 305  
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt  
 1075  
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val  
 310 315 320 325  
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc  
 1123  
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg  
 330 335 340  
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att  
 1171  
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile  
 345 350 355  
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg  
 1219  
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val  
 360 365 370  
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca  
 1267  
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr  
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 1296  
 Ile Ala  
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 <212> PRT  
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 35 40 45  
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln  
 50 55 60  
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val  
 65 70 75 80  
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala  
 85 90 95  
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu  
 100 105 110  
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg

115	120	125
Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu 130 135 140		
Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro 145 150 155 160		
Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys 165 170 175		
Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro 180 185 190		
Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys 195 200 205		
Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp 210 215 220		
Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln 225 230 235 240		
His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly 245 250 255		
Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu 260 265 270		
Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val 275 280 285		
Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe 290 295 300		
Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala 305 310 315 320		
Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly 325 330 335		
Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe 340 345 350		
Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu 355 360 365		
Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys 370 375 380		
Ala Ile Ala Glu Thr Ile Ala 385 390		

&lt;210&gt; 329

&lt;211&gt; 1491

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1468)

&lt;223&gt; RXS02970

&lt;400&gt; 329

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aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttattttaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
                                   Leu Ala Leu Lys Gly
                                   1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
              10              15              20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
              25              30              35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
              40              45              50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
              55              60              65

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Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
              70              75              80              85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
              90              95              100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
              105              110              115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
              120              125              130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
              135              140              145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
              150              155              160              165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
              170              175              180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
              185              190              195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
              200              205              210

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cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787  
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala  
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835  
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro  
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883  
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile  
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931  
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys  
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979  
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile  
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc  
 1027  
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile  
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc  
 1075  
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser  
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag  
 1123  
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys  
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct  
 1171  
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala  
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa  
 1219  
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu  
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca  
 1267  
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala  
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
 1315  
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
 390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac  
 1363  
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
 410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg  
 1411  
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
                   425                                  430                                  435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg  
 1459  
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
                   440                                  445                                  450

gcg ttg ttc taagttttct agataacaag gcc  
 1491  
 Ala Leu Phe  
                   455

<210> 330  
 <211> 456  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 330  
 Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
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 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
                   20                                  25                                  30  
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
                   35                                  40                                  45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
                   50                                  55                                  60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
   65                                  70                                  75                                  80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
                   85                                  90                                  95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
                   100                                  105                                  110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
                   115                                  120                                  125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
                   130                                  135                                  140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
   145                                  150                                  155                                  160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
                   165                                  170                                  175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
                   180                                  185                                  190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
                   195                                  200                                  205



Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
 370 375 380  
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
 385 390 395 400  
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser  
 405 410 415  
 Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu  
 420 425 430  
 Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu  
 435 440 445  
 Leu Thr Phe Ala Gly Ala Leu Phe  
 450 455

&lt;210&gt; 331

&lt;211&gt; 1330

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1330)

&lt;223&gt; FRXA01009

&lt;400&gt; 331

aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttattttaag acttcataat attttgggga gtgaactggt	ttg gca ttg aag ggt	115
	Leu Ala Leu Lys Gly	
	1 5	
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163	
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala		
	10 15 20	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211	
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe		
	25 30 35	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259	
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala		
	40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307	
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp		
	55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355	
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg		
	70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403	
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn		
	90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451	
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val		
	105 110 115	
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499	
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly		
	120 125 130	
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547	
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly		
	135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595	
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly		
	150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643	
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr		
	170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691	
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser		
	185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739	
Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys Glu Arg Ala Leu Lys		
	200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787	
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala		
	215 220 225	

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atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca      835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
230                      235                      240                      245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc      883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
                250                      255                      260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa      931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
                265                      270                      275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc      979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
                280                      285                      290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
    295                      300                      305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
310                      315                      320                      325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
                330                      335                      340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
                345                      350                      355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
    360                      365                      370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
    375                      380                      385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390                      395                      400                      405

ttc aag gaa cgc ggc
1330
Phe Lys Glu Arg Gly
                410

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&lt;210&gt; 332

&lt;211&gt; 410

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 332

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
 1 5 10 15  
 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
 20 25 30  
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255  
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
 370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala  
 385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly  
 405 410

<210> 333  
 <211> 1080  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1057)  
 <223> RXA02158

<400> 333  
 aacattatcc gtttgacccc gccgctggtg atcaccgacg aagaaatcgc agacgcagtc 60

aaggctattg ccgagacaat cgcataaagg actcaaactt atg act tca caa cca 115  
 Met Thr Ser Gln Pro  
 1 5

cag gtt cgc cat ttt ctg gct gat gat gat ctc acc cct gca gag cag 163  
 Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu Thr Pro Ala Glu Gln  
 10 15 20

gca gag gtt ttg acc cta gcc gca aag ctc aag gca gcg ccg ttt tcg 211  
 Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys Ala Ala Pro Phe Ser  
 25 30 35

gag cgt cca ctc gag gga cca aag tcc gtt gca gtt ctt ttt gat aag 259  
 Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala Val Leu Phe Asp Lys  
 40 45 50

act tca act cgt act cgc ttc tcc ttc gac gcg ggc atc gct cat ttg 307  
 Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala Gly Ile Ala His Leu  
 55 60 65

ggg gga cac gcc atc gtc gtg gat tcc ggt agc tca cag atg ggt aag 355  
 Gly Gly His Ala Ile Val Val Asp Ser Gly Ser Ser Gln Met Gly Lys  
 70 75 80 85

ggc gag tcc ctg cag gac acc gca gct gta ttg tcc cgc tac gtg gaa 403  
 Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu Ser Arg Tyr Val Glu  
 90 95 100

gca att gtg tgg cgc acc tac gca cac agc aat ttc cac gcc atg gcg 451  
 Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn Phe His Ala Met Ala  
 105 110 115

gag acg tcc act gtg ccg ctg gtg aac tcc ttg tcc gat gat ctg cac 499  
 Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu Ser Asp Asp Leu His  
 120 125 130

cca tgc cag att ctg gct gat ctg cag act atc gtg gaa aac ctc agc 547  
 Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile Val Glu Asn Leu Ser  
 135 140 145

cct gaa gaa ggc cca gca ggc ctt aag ggt aag aag gct gtg tac ctg 595  
 Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys Lys Ala Val Tyr Leu  
 150 155 160 165

ggc gat ggc gac aac aac atg gcc aac tcc tac atg att ggc ttt gcc 643  
 Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr Met Ile Gly Phe Ala  
 170 175 180

acc gcg ggc atg gat att tcc atc atc gct cct gaa ggg ttc cag cct 691  
 Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro Glu Gly Phe Gln Pro  
 185 190 195

cgt gcg gaa ttc gtg gag cgc gcg gaa aag cgt ggc cag gaa acc ggc 739  
 Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg Gly Gln Glu Thr Gly  
 200 205 210

gcg aag gtt gtt gtc acc gac agc ctc gac gag gtt gcc ggc gcc gat 787  
 Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu Val Ala Gly Ala Asp  
 215 220 225

gtt gtc atc acc gat acc tgg gta tcc atg ggt atg gaa aac gac ggc 835  
 Val Val Ile Thr Asp Thr Trp Val Ser Met Gly Met Glu Asn Asp Gly  
 230 235 240 245

atc gat cgc acc aca cct ttc gtt cct tac cag gtc aac gat gag gtc 883  
 Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln Val Asn Asp Glu Val  
 250 255 260

atg gcg aaa gct aac gac ggc gcc atc ttc ctg cac tgc ctt cct gcc 931  
 Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu His Cys Leu Pro Ala  
 265 270 275

tac cgt ggc aaa gaa gtg gca gcc tcc gtg att gat gga cca gcg tcc 979  
 Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser  
 280 285 290

aaa gtt ttc gat gaa gca gaa aac cgc ctc cac gct cag aaa gca ctg  
 1027  
 Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His Ala Gln Lys Ala Leu  
 295 300 305

ctg gtg tgg ctg ctg gcc aac cag ccg agg taagacatgt cccttggtc  
 1077  
 Leu Val Trp Leu Leu Ala Asn Gln Pro Arg  
 310 315

aac  
 1080

&lt;210&gt; 334

&lt;211&gt; 319

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 334

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Met Thr Ser Gln Pro Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu
 1           5           10           15

Thr Pro Ala Glu Gln Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys
          20           25           30

Ala Ala Pro Phe Ser Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala
          35           40           45

Val Leu Phe Asp Lys Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala
          50           55           60

Gly Ile Ala His Leu Gly Gly His Ala Ile Val Val Asp Ser Gly Ser
 65           70           75           80

Ser Gln Met Gly Lys Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu
          85           90           95

Ser Arg Tyr Val Glu Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn
          100          105          110

Phe His Ala Met Ala Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu
          115          120          125

Ser Asp Asp Leu His Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile
          130          135          140

Val Glu Asn Leu Ser Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys
          145          150          155          160

Lys Ala Val Tyr Leu Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr
          165          170          175

Met Ile Gly Phe Ala Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro
          180          185          190

Glu Gly Phe Gln Pro Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg
          195          200          205

Gly Gln Glu Thr Gly Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu
          210          215          220

Val Ala Gly Ala Asp Val Val Ile Thr Asp Thr Trp Val Ser Met Gly
          225          230          235          240

Met Glu Asn Asp Gly Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln
          245          250          255

Val Asn Asp Glu Val Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu
          260          265          270

His Cys Leu Pro Ala Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile
          275          280          285

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Asp Gly Pro Ala Ser Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His  
 290 295 300

Ala Gln Lys Ala Leu Leu Val Trp Leu Leu Ala Asn Gln Pro Arg  
 305 310 315

<210> 335

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> RXA02160

<400> 335

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ccacggctgg caaggaactt aaaatgaagg agcacacctc atg act aac cgc atc 115  
 Met Thr Asn Arg Ile  
 1 5

ggt ctt gca tac tcc ggc ggt ctg gac acc act gtg gca att cca tac 163  
 Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr Val Ala Ile Pro Tyr  
 10 15 20

ctg aag aag atg att gat ggt gaa gtc atc gca gtt tcc ctc gac ctg 211  
 Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala Val Ser Leu Asp Leu  
 25 30 35

ggc cag ggt gga gag aac atg gac aac gtt cgc cag cgt gca ttg gat 259  
 Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg Gln Arg Ala Leu Asp  
 40 45 50

gcc ggt gca gct gag tcc atc gtt gtt gat gca aag gat gag ttc gct 307  
 Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala Lys Asp Glu Phe Ala  
 55 60 65

gag gag tac tgc ctg cca acc atc aag gca aac ggc atg tac atg aag 355  
 Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn Gly Met Tyr Met Lys  
 70 75 80 85

cag tac cca ctg gtt tct gca atc tcc cgc cca ctg atc gtc aag cac 403  
 Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro Leu Ile Val Lys His  
 90 95 100

ctc gtt gag gct ggc aag cag ttc aac ggt acc cac gtt gca cac ggc 451  
 Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr His Val Ala His Gly  
 105 110 115

tgc act ggt aag ggc aac gac cag gtt cgt ttc gag gtc ggc ttc atg 499  
 Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val Gly Phe Met  
 120 125 130

gac acc gat cca aac ctg gag atc att gca cct gct cgt gac ttc gca 547  
 Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro Ala Arg Asp Phe Ala  
 135 140 145

tgg acc cgc gac aag gct atc gcc ttc gcc gag gag aac aac gtt cca 595



Trp	Thr	Arg	Asp	Lys	Ala	Ile	Ala	Phe	Ala	Glu	Glu	Asn	Asn	Val	Pro		
150					155					160					165		
atc	gag	cag	tcc	gtg	aag	tcc	cca	ttc	tcc	atc	gac	cag	aac	gtc	tgg	643	
Ile	Glu	Gln	Ser	Val	Lys	Ser	Pro	Phe	Ser	Ile	Asp	Gln	Asn	Val	Trp		
				170					175					180			
ggc	cgc	gct	att	gag	acc	ggc	tac	ctg	gaa	gat	ctg	tgg	aac	gct	cca	691	
Gly	Arg	Ala	Ile	Glu	Thr	Gly	Tyr	Leu	Glu	Asp	Leu	Trp	Asn	Ala	Pro		
				185				190					195				
acc	aag	gac	atc	tac	gca	tac	acc	gag	gat	cca	gct	ctg	ggc	aac	gct	739	
Thr	Lys	Asp	Ile	Tyr	Ala	Tyr	Thr	Glu	Asp	Pro	Ala	Leu	Gly	Asn	Ala		
		200					205					210					
cca	gat	gag	gtc	atc	atc	tcc	ttc	gag	ggc	ggc	aag	cca	gtc	tcc	atc	787	
Pro	Asp	Glu	Val	Ile	Ile	Ser	Phe	Glu	Gly	Gly	Lys	Pro	Val	Ser	Ile		
		215				220					225						
gat	ggc	cgt	cca	gtc	tcc	gta	ctg	cag	gct	att	gaa	gag	ctg	aac	cgt	835	
Asp	Gly	Arg	Pro	Val	Ser	Val	Leu	Gln	Ala	Ile	Glu	Glu	Leu	Asn	Arg		
230					235					240					245		
cgt	gca	ggc	gca	cag	ggc	gtt	ggc	cgc	ctt	gac	atg	gtt	gag	gac	cgt	883	
Arg	Ala	Gly	Ala	Gln	Gly	Val	Gly	Arg	Leu	Asp	Met	Val	Glu	Asp	Arg		
				250				255						260			
ctc	gtg	ggc	atc	aag	tcc	cgc	gaa	atc	tac	gaa	gca	cca	ggc	gca	atc	931	
Leu	Val	Gly	Ile	Lys	Ser	Arg	Glu	Ile	Tyr	Glu	Ala	Pro	Gly	Ala	Ile		
			265					270					275				
gca	ctg	att	aag	gct	cac	gag	gct	ttg	gaa	gat	gtc	acc	atc	gag	cgc	979	
Ala	Leu	Ile	Lys	Ala	His	Glu	Ala	Leu	Glu	Asp	Val	Thr	Ile	Glu	Arg		
		280				285						290					
gaa	ctg	gct	cgc	tac	aag	cgc	ggc	gtt	gac	gca	cgt	tgg	gct	gag	gaa		
1027																	
Glu	Leu	Ala	Arg	Tyr	Lys	Arg	Gly	Val	Asp	Ala	Arg	Trp	Ala	Glu	Glu		
		295				300					305						
gta	tac	gac	ggc	ctg	tgg	ttc	gga	cct	ctg	aag	cgc	tcc	ctg	gac	gca		
1075																	
Val	Tyr	Asp	Gly	Leu	Trp	Phe	Gly	Pro	Leu	Lys	Arg	Ser	Leu	Asp	Ala		
310					315					320					325		
ttc	att	gat	tcc	acc	cag	gag	cac	gtc	acc	ggc	gat	atc	cgc	atg	gtt		
1123																	
Phe	Ile	Asp	Ser	Thr	Gln	Glu	His	Val	Thr	Gly	Asp	Ile	Arg	Met	Val		
				330					335					340			
ctg	cac	gca	ggc	tcc	atc	acc	atc	aat	ggc	cgt	cgt	tcc	agc	cac	tcc		
1171																	
Leu	His	Ala	Gly	Ser	Ile	Thr	Ile	Asn	Gly	Arg	Arg	Ser	Ser	His	Ser		
			345					350					355				
ctg	tac	gac	ttc	aac	ctg	gct	acc	tac	gac	acc	ggc	gac	acc	ttc	gac		
1219																	
Leu	Tyr	Asp	Phe	Asn	Leu	Ala	Thr	Tyr	Asp	Thr	Gly	Asp	Thr	Phe	Asp		
		360					365					370					

cag acc ctg gct aag ggc ttt gtc cag ctg cac ggt ctg tcc tcc aag  
1267

Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His Gly Leu Ser Ser Lys  
375 380 385

atc gct aac aag cgc gat cgc gaa gct ggc aac aac taagccacct

1313

Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn Asn  
390 395 400

tttcaagcat cca

1326

<210> 336

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

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Val Ala Ile Pro Tyr Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala  
20 25 30

Val Ser Leu Asp Leu Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg  
35 40 45

Gln Arg Ala Leu Asp Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala  
50 55 60

Lys Asp Glu Phe Ala Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn  
65 70 75 80

Gly Met Tyr Met Lys Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro  
85 90 95

Leu Ile Val Lys His Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr  
100 105 110

His Val Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe  
115 120 125

Glu Val Gly Phe Met Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro  
130 135 140

Ala Arg Asp Phe Ala Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu  
145 150 155 160

Glu Asn Asn Val Pro Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile  
165 170 175

Asp Gln Asn Val Trp Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp  
180 185 190

Leu Trp Asn Ala Pro Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro  
195 200 205

Ala Leu Gly Asn Ala Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly  
210 215 220

Lys Pro Val Ser Ile Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile  
 225 230 235 240  
 Glu Glu Leu Asn Arg Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp  
 245 250 255  
 Met Val Glu Asp Arg Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu  
 260 265 270  
 Ala Pro Gly Ala Ile Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp  
 275 280 285  
 Val Thr Ile Glu Arg Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala  
 290 295 300  
 Arg Trp Ala Glu Glu Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys  
 305 310 315 320  
 Arg Ser Leu Asp Ala Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly  
 325 330 335  
 Asp Ile Arg Met Val Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg  
 340 345 350  
 Arg Ser Ser His Ser Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr  
 355 360 365  
 Gly Asp Thr Phe Asp Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His  
 370 375 380  
 Gly Leu Ser Ser Lys Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn  
 385 390 395 400  
 Asn

<210> 337  
 <211> 1554  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1531)  
 <223> RXN02162

<400> 337  
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 gactagaact tcaagtattt agaaagtaga agaacaccac atg gaa cag cac gga 115  
 Met Glu Gln His Gly  
 1 5  
 acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163  
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser  
 10 15 20  
 gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211  
 Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu

25						30						35						
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Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His			
		40					45					50						
caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg	307		
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly			
		55				60					65							
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggg	ccg	ctg	355		
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu			
		70			75					80					85			
cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggg	gtg	att	gac	403		
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp			
				90					95					100				
cgc	gtt	ggg	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggg	cgt	tcc	cgc	451		
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg			
			105					110					115					
aac	gac	cag	gtg	gca	acc	ctg	ttc	cgc	atg	tgg	gtc	cgc	gac	gca	gtg	499		
Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val			
		120					125					130						
cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc	547		
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala			
		135				140					145							
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc	595		
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe			
		150			155					160					165			
cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca	643		
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala			
				170					175					180				
cag	cct	ttg	ctg	cgc	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt	691		
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg			
			185					190					195					
ctt	gcg	gtg	tct	cct	tac	ggg	tcc	ggc	gca	ctt	gct	ggg	tcc	tct	ttg	739		
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu			
		200					205					210						
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca	787		
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala			
		215				220					225							
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa	835		
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu			
		230			235					240					245			
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	gtg	gat	atg	tcc	cgc	ttg	gct	883		
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Val	Asp	Met	Ser	Arg	Leu	Ala			
			250					255						260				
gaa	gaa	atc	atc	gca	tgg	tgc	acc	cca	gaa	ttt	ggg	tac	atc	acc	ttg	931		
Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe	Gly	Tyr	Ile	Thr	Leu			
			265					270					275					

tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 979  
 Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn  
 280 285 290

cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt  
 1027  
 Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly  
 295 300 305

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac  
 1075  
 Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr  
 310 315 320 325

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg  
 1123  
 Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala  
 330 335 340

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg  
 1171  
 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu  
 345 350 355

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc  
 1219  
 Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr  
 360 365 370

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc  
 1267  
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe  
 375 380 385

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc  
 1315  
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser  
 390 395 400 405

agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt  
 1363  
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val  
 410 415 420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt  
 1411  
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly  
 425 430 435

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt  
 1459  
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val  
 440 445 450

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag  
 1507  
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu  
 455 460 465

tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg

1554

Trp Ala Arg Ala Gly Val Arg Arg

470

475

<210> 338

<211> 477

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 338

Met Glu Gln His Gly Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe  
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Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His  
20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His  
35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala  
50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly  
65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu  
85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg  
100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp  
115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val  
130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro  
145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln  
165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg  
180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu  
195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu  
210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg  
225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp  
245 250 255

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe

260 265 270  
 Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met  
 275 280 285  
 Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser  
 290 295 300  
 Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala  
 305 310 315 320  
 Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile  
 325 330 335  
 Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly  
 340 345 350  
 Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala  
 355 360 365  
 Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg  
 370 375 380  
 Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val  
 385 390 395 400  
 Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu  
 405 410 415  
 Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val  
 420 425 430  
 Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr  
 435 440 445  
 Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser  
 450 455 460  
 Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg  
 465 470 475

&lt;210&gt; 339

&lt;211&gt; 906

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(883)

&lt;223&gt; FRXA02161

&lt;400&gt; 339

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gactagaact tcaagtattt agaaagtaga agaacaccac atg gaa cag cac gga 115  
 Met Glu Gln His Gly  
 1 5

acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163  
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser

				10				15				20							
gag	gcc	atg	ttc	gcc	ttg	agt	gtc	tcc	act	cat	ttc	gac	tgg	gtt	ttg	211			
Glu	Ala	Met	Phe	Ala	Leu	Ser	Val	Ser	Thr	His	Phe	Asp	Trp	Val	Leu				
25								30				35							
gcc	cct	tat	gat	gtg	ttg	gcc	tcc	aag	gca	cac	gcc	aag	gtt	ttg	cac	259			
Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His				
40								45				50							
caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg	307			
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly				
55								60				65							
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggg	ccg	ctg	355			
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu				
70				75				80				85							
cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggg	gtg	att	gac	403			
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp				
90								95				100							
cgc	gtt	ggg	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggg	cgt	tcc	cgc	451			
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg				
105								110				115							
aac	gac	cag	gtg	gca	acc	ctg	ttc	cgc	atg	tgg	gtc	cgc	gac	gca	gtg	499			
Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val				
120								125				130							
cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc	547			
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala				
135				140				145											
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc	595			
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe				
150				155				160				165							
cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca	643			
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala				
170								175				180							
cag	cct	ttg	ctg	cgc	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt	691			
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg				
185								190				195							
ctt	gcg	gtg	tct	cct	tac	ggg	tcc	ggc	gca	ctt	gct	ggg	tcc	tct	ttg	739			
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu				
200								205				210							
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca	787			
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala				
215				220				225											
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa	835			
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu				
230				235				240				245							
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	ngt	gga	tat	gtc	ccg	ctt	ggc	883			
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly	Tyr	Val	Pro	Leu	Gly				
250								255				260							



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906

&lt;210&gt; 340

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 340

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Ser	Gly	Gly	Pro	Ser	Glu	Ala	Met	Phe	Ala	Leu	Ser	Val	Ser	Thr	His
			20					25					30		

Phe	Asp	Trp	Val	Leu	Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His
	35						40					45			

Ala	Lys	Val	Leu	His	Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala
	50					55					60				

Thr	Met	Leu	Ala	Gly	Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly
65					70					75					80

Thr	Phe	Gly	Pro	Leu	Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu
				85					90					95	

Arg	Gly	Val	Ile	Asp	Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg
			100					105					110		

Ala	Gly	Arg	Ser	Arg	Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp
		115					120						125		

Val	Arg	Asp	Ala	Val	Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val
	130					135					140				

Asp	Ala	Leu	Ser	Ala	Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro
145					150					155					160

Gly	Lys	Thr	His	Phe	Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln
				165					170					175	

Leu	Leu	Ala	His	Ala	Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg
			180					185					190		

Asp	Leu	Asp	Lys	Arg	Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu
		195					200					205			

Ala	Gly	Ser	Ser	Leu	Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu
	210					215						220			

Gly	Phe	Asp	Ser	Ala	Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg
225					230					235					240

Asp	Phe	Ala	Ser	Glu	Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly
				245					250					255	

Tyr	Val	Pro	Leu	Gly
			260	

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<210> 341
<211> 786
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(763)  
<223> FRXA02162
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tctgaaaccg ccttcgtgct ggcgcagctt gcangtggat																
											atg	tcc	cgc	ttg	gct	115
											Met	Ser	Arg	Leu	Ala	
											1				5	
gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg																163
Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe	Gly	Tyr	Ile	Thr	Leu	
				10					15					20		
tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac																211
Ser	Asp	Ser	Trp	Ser	Thr	Gly	Ser	Ser	Ile	Met	Pro	Gln	Lys	Lys	Asn	
			25					30					35			
cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt																259
Pro	Asp	Val	Ala	Glu	Leu	Thr	Arg	Gly	Lys	Ser	Gly	Arg	Leu	Ile	Gly	
		40					45					50				
aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac																307
Asn	Leu	Thr	Gly	Leu	Leu	Ala	Thr	Leu	Lys	Ala	Gln	Pro	Leu	Ala	Tyr	
	55					60					65					
aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg																355
Asn	Arg	Asp	Leu	Gln	Glu	Asp	Lys	Glu	Pro	Ile	Val	Asp	Ser	Val	Ala	
70				75					80						85	
cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg																403
Gln	Leu	Asn	Leu	Leu	Leu	Pro	Ala	Met	Thr	Gly	Leu	Val	Ser	Thr	Leu	
			90						95					100		
acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc																451
Thr	Phe	Asn	Thr	Glu	Arg	Met	Arg	Glu	Leu	Ala	Pro	Ala	Gly	Phe	Thr	
			105					110					115			
ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc																499
Leu	Ala	Thr	Asp	Leu	Ala	Glu	Trp	Met	Val	Arg	Gln	Gly	Val	Pro	Phe	
		120				125					130					
cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc																547
Arg	Glu	Ala	His	Glu	Ala	Ser	Gly	Ala	Cys	Val	Arg	Ile	Ala	Glu	Ser	
	135					140				145						
agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt																595
Arg	Gly	Val	Asp	Leu	Ile	Asp	Leu	Thr	Asp	Glu	Glu	Leu	Ser	Gly	Val	
150					155					160					165	
gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt																643
Asp	Ala	Arg	Leu	Thr	Pro	Glu	Val	Arg	Glu	Val	Leu	Thr	Ile	Asp	Gly	
			170						175					180		

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 691  
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val  
                   185                                  190                                  195

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739  
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu  
                   200                                  205                                  210

tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg 786  
 Trp Ala Arg Ala Gly Val Arg Arg  
                   215                                  220

<210> 342

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe  
           1                                  5                                  10                                  15

Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met  
                   20                                  25                                  30

Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser  
                   35                                  40                                  45

Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala  
           50                                  55                                  60

Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile  
           65                                  70                                  75                                  80

Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly  
                   85                                  90                                  95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala  
                   100                                  105                                  110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg  
                   115                                  120                                  125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val  
           130                                  135                                  140

Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu  
           145                                  150                                  155                                  160

Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val  
                   165                                  170                                  175

Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr  
                   180                                  185                                  190

Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser  
                   195                                  200                                  205

Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg  
           210                                  215                                  220

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<210> 343
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1246)
<223> RXA02262
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tcgataagca aaaaatcgct gatactcgaa aggcctcaaa atg acc gca acc tac																	115
Met Thr Ala Thr Tyr																	5
1																	
acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg																	163
Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met																	
10 15 20																	
atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag																	211
Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu																	
25 30 35																	
gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg																	259
Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu																	
40 45 50																	
aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa																	307
Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu																	
55 60 65																	
ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg																	355
Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met																	
70 75 80 85																	
ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac																	403
Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr																	
90 95 100																	
gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac																	451
Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His																	
105 110 115																	
acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg																	499
Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met																	
120 125 130																	
tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg																	547
Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val																	
135 140 145																	
ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc																	595
Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val																	
150 155 160 165																	
gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag																	643
Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu																	

	170	175	180	
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc				691
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly				
	185	190	195	
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa				739
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu				
	200	205	210	
gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc				787
Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile				
	215	220	225	
gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca				835
Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro				
	230	235	240	245
tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca				883
Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro				
	250	255	260	
gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc				931
Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu				
	265	270	275	
gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc				979
Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly				
	280	285	290	
cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac				
1027				
Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp				
	295	300	305	
ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc				
1075				
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly				
	310	315	320	325
gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc				
1123				
Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile				
	330	335	340	
atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca				
1171				
Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala				
	345	350	355	
acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg				
1219				
Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu				
	360	365	370	
aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg				
1266				
Asn Leu Trp Glu Ser Pro Ala Leu Ala				
	375	380		

aaa  
1269

<210> 344  
<211> 382  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 344

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Ser	Glu	Pro	Asp	Met	Ile	Ala	Ala	Gly	Val	Lys	Asp	Val	Ala	Gln	Cys	20	25	30	
Val	Asp	Val	Met	Glu	Glu	Thr	Leu	Val	Leu	Leu	Ala	Gln	Gly	Asp	Tyr	35	40	45	
Lys	Met	Ala	Gly	Leu	Asn	Ser	Asn	Ser	His	Gly	Ala	Met	Ile	Thr	Phe	50	55	60	
Pro	Glu	Asn	Pro	Glu	Phe	Glu	Gly	Met	Pro	Lys	Asp	Gly	Pro	Asp	Arg	65	70	75	80
Arg	Phe	Met	Ala	Met	Pro	Ala	Tyr	Leu	Gly	Gly	Arg	Phe	Lys	Asn	Thr	85	90	95	
Gly	Val	Lys	Trp	Tyr	Gly	Ser	Asn	Ala	Glu	Asn	Lys	Ala	Ser	Gly	Leu	100	105	110	
Pro	Arg	Ser	Ile	His	Thr	Phe	Val	Leu	Asn	Asp	Thr	Val	Thr	Gly	Ala	115	120	125	
Pro	Lys	Ala	Ile	Met	Ser	Ala	Asn	Leu	Leu	Ser	Ala	Tyr	Arg	Thr	Gly	130	135	140	
Ala	Val	Pro	Gly	Val	Gly	Val	Lys	His	Leu	Ala	Val	Ala	Asp	Ala	Thr	145	150	155	160
Thr	Leu	Ala	Val	Val	Gly	Pro	Gly	Val	Met	Ala	Lys	Thr	Ile	Thr	Glu	165	170	175	
Ala	Cys	Ile	Ala	Glu	Arg	Pro	Gly	Ile	Thr	Thr	Ile	Lys	Ile	Lys	Gly	180	185	190	
Arg	Ser	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Ala	Thr	Trp	Ala	Leu	Glu	Lys	195	200	205	
Phe	Pro	Glu	Ile	Glu	Val	Val	Ala	Val	Gly	Ser	Glu	Glu	Asp	Val	Val	210	215	220	
Lys	Asp	Ala	Asp	Ile	Val	Ile	Ala	Ala	Thr	Thr	Thr	Asp	Ala	Ala	Gly	225	230	235	240
Ser	Ser	Ala	Phe	Pro	Tyr	Phe	Lys	Lys	Glu	Trp	Leu	Lys	Pro	Gly	Ala	245	250	255	
Leu	Leu	Leu	Leu	Pro	Ala	Ala	Gly	Arg	Phe	Asp	Asp	Ala	Tyr	Leu	Leu	260	265	270	

Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp  
 275 280 285  
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly  
 290 295 300  
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys  
 305 310 315 320  
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr  
 325 330 335  
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu  
 340 345 350  
 Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly  
 355 360 365  
 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala  
 370 375 380

&lt;210&gt; 345

&lt;211&gt; 1065

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1042)

&lt;223&gt; RXA00219

&lt;400&gt; 345

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cacaagcact aaaacagcat taaagaaaga aagctttttc gtg gcc cgt aag aaa 115  
 Val Ala Arg Lys Lys  
 1 5

aac acg tcc gat caa tcc cgc tcc caa gct gcc aac acg ccc att gct 163  
 Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala Asn Thr Pro Ile Ala  
 10 15 20

ggc acc tat gag ggt gaa tat tcc gtc atc gag ttg gag gcc gat tcc 211  
 Gly Thr Tyr Glu Gly Glu Tyr Ser Val Ile Glu Leu Glu Ala Asp Ser  
 25 30 35

tac acc acc gat ggc tgg ttg atc agc att aat ggc gtg ccc agc tct 259  
 Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn Gly Val Pro Ser Ser  
 40 45 50

cat att gtc ctg ggg caa ccg cag gca ctg gaa ttt gag tac atg cgg 307  
 His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu Phe Glu Tyr Met Arg  
 55 60 65

tgg atc gct acc ggc gct cgg gcg ttc atc gat gcg cat cag gat gca 355  
 Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp Ala His Gln Asp Ala  
 70 75 80 85

tcc aag ctg cgg att act cac ctc ggc ggc ggt gcg tgc acg atg gcc 403  
 Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly Ala Cys Thr Met Ala

	90	95	100	
agg tat ttc gcg gat gtt tac ccg cag tca cgc aac act gtc gtg gaa				451
Arg Tyr Phe Ala Asp Val Tyr Pro Gln Ser Arg Asn Thr Val Val Glu	105	110	115	
ttg gat gca gag ctt gcc cgc ctg tcg cgt gaa tgg ttc gac att ccg				499
Leu Asp Ala Glu Leu Ala Arg Leu Ser Arg Glu Trp Phe Asp Ile Pro	120	125	130	
cgc gcg cca cgg gta aag att cgt gtg gat gat gcc cga atg gtg gca				547
Arg Ala Pro Arg Val Lys Ile Arg Val Asp Asp Ala Arg Met Val Ala	135	140	145	
gaa tct ttc act ccc gca agc cgc gat gtg atc atc cgt gac gtt ttt				595
Glu Ser Phe Thr Pro Ala Ser Arg Asp Val Ile Ile Arg Asp Val Phe	150	155	160	165
gcc gga gct atc acg ccg cag aac ttc acc acc gtg gag ttc ttt gag				643
Ala Gly Ala Ile Thr Pro Gln Asn Phe Thr Thr Val Glu Phe Phe Glu	170	175	180	
cac tgt cac cgt ggc ctt gct ccc ggc gga ttg tac gtt gcc aac tgt				691
His Cys His Arg Gly Leu Ala Pro Gly Gly Leu Tyr Val Ala Asn Cys	185	190	195	
ggc gat cat tcg gat ctg cgc gga gct aaa tct gag ctc gcg gga atg				739
Gly Asp His Ser Asp Leu Arg Gly Ala Lys Ser Glu Leu Ala Gly Met	200	205	210	
atg gag gtg ttc gag cac gtc gcg gtc atc gcc gat ccc ccg atg ctt				787
Met Glu Val Phe Glu His Val Ala Val Ile Ala Asp Pro Pro Met Leu	215	220	225	
aaa ggg cgc cgt tac ggc aac atc att ttg atg ggt tca gac acc gag				835
Lys Gly Arg Arg Tyr Gly Asn Ile Ile Leu Met Gly Ser Asp Thr Glu	230	235	240	245
ttc ttt agc tcc aac agc acg gaa gcg tcc gcg att acc cgt gag ctt				883
Phe Phe Ser Ser Asn Ser Thr Glu Ala Ser Ala Ile Thr Arg Glu Leu	250	255	260	
ctt ggc ggc ggc gtt cca gcg cag tac aag gat gaa tcc tgg gtg cgg				931
Leu Gly Gly Gly Val Pro Ala Gln Tyr Lys Asp Glu Ser Trp Val Arg	265	270	275	
aaa ttc gcc tcg gga gcc cag gcc cgc cac gat ggg gtc tct acc ctc				979
Lys Phe Ala Ser Gly Ala Gln Ala Arg His Asp Gly Val Ser Thr Leu	280	285	290	
caa atg ccg agt gat act cca caa cac cct gcg gaa acg ccg gag cat				1027
Gln Met Pro Ser Asp Thr Pro Gln His Pro Ala Glu Thr Pro Glu His	295	300	305	
tca aac aca cag cca taaaaaatc cgctggcgcg tcc				1065
Ser Asn Thr Gln Pro				310



&lt;210&gt; 346

&lt;211&gt; 314

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 346

Val	Ala	Arg	Lys	Lys	Asn	Thr	Ser	Asp	Gln	Ser	Arg	Ser	Gln	Ala	Ala	
1				5					10					15		
Asn	Thr	Pro	Ile	Ala	Gly	Thr	Tyr	Glu	Gly	Glu	Tyr	Ser	Val	Ile	Glu	
			20					25					30			
Leu	Glu	Ala	Asp	Ser	Tyr	Thr	Thr	Asp	Gly	Trp	Leu	Ile	Ser	Ile	Asn	
		35					40					45				
Gly	Val	Pro	Ser	Ser	His	Ile	Val	Leu	Gly	Gln	Pro	Gln	Ala	Leu	Glu	
	50					55					60					
Phe	Glu	Tyr	Met	Arg	Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp	
65					70					75					80	
Ala	His	Gln	Asp	Ala	Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly	
				85					90					95		
Ala	Cys	Thr	Met	Ala	Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	
			100					105					110			
Asn	Thr	Val	Val	Glu	Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	
		115					120					125				
Trp	Phe	Asp	Ile	Pro	Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	
	130					135						140				
Ala	Arg	Met	Val	Ala	Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	
145					150					155					160	
Ile	Arg	Asp	Val	Phe	Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	
				165					170					175		
Val	Glu	Phe	Phe	Glu	His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	
			180					185					190			
Tyr	Val	Ala	Asn	Cys	Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	
		195					200					205				
Glu	Leu	Ala	Gly	Met	Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	
	210					215					220					
Asp	Pro	Pro	Met	Leu	Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met	
225					230					235					240	
Gly	Ser	Asp	Thr	Glu	Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala	
				245					250					255		
Ile	Thr	Arg	Glu	Leu	Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp	
			260					265					270			
Glu	Ser	Trp	Val	Arg	Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp	
		275					280					285				
Gly	Val	Ser	Thr	Leu	Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala	

290 295 300

Glu Thr Pro Glu His Ser Asn Thr Gln Pro  
305 310

<210> 347  
<211> 1662  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1639)  
<223> RXA01508

<400> 347  
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ccgccgtcat cttgatcgtg gtgggaaccg taaacgctgc atg tct gat tta gga 115  
Met Ser Asp Leu Gly  
1 5  
ccc atc tgg cgc tgg ctg tta tta gtt tcc gtc tcc att tgt gcg gca 163  
Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala  
10 15 20  
tcg ggg ctg gtc tat gag cta gcc ctg gta tcg ctt tcc acc agc ttg 211  
Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu  
25 30 35  
aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259  
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val  
40 45 50  
gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307  
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp  
55 60 65  
cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355  
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly  
70 75 80 85  
ggt tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403  
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln  
90 95 100  
tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc 451  
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val  
105 110 115  
ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc 499  
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu  
120 125 130  
gcc gac gcc aaa acc aca gga tct ctg gtt gcc acc ttg aat gct gct 547  
Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala  
135 140 145  
gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg 595  
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu

150	155	160	165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc				643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Ala Gly Met Ile				
	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu				
	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala				
	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala				
	215	220	225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln				
	230	235	240	245
tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg				
	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg				
	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser				
	280	285	290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc				
1027				
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu				
	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				
1075				
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val				
	310	315	320	325
atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg				
1123				
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met				
	330	335	340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				
1171				
Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu				
	345	350	355	
cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat				
1219				
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp				
	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				
1267				

Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu  
 375 380 385

ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg  
 1315

Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val  
 390 395 400 405

gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt  
 1363

Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val  
 410 415 420

gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac  
 1411

Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His  
 425 430 435

gtg cat gtt ccc aca ttt ggc gac tgg ggc ttc caa ctg tgt ggc cct  
 1459

Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro  
 440 445 450

gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc  
 1507

Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe  
 455 460 465

ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat  
 1555

Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn  
 470 475 480 485

cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg  
 1603

Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val  
 490 495 500

gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac  
 1649

Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp  
 505 510

gatgcgctgt gtg  
 1662

<210> 348

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Ser Asp Leu Gly Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val  
 1 5 10 15

Ser Ile Cys Ala Ala Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser  
 20 25 30

Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile  
 35 40 45

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys  
 50 55 60  
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu  
 65 70 75 80  
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe  
 85 90 95  
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala  
 100 105 110  
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile  
 115 120 125  
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala  
 130 135 140  
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala  
 145 150 155 160  
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala  
 165 170 175  
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val  
 180 185 190  
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val  
 195 200 205  
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser  
 210 215 220  
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val  
 225 230 235 240  
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg  
 245 250 255  
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr  
 260 265 270  
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn  
 275 280 285  
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala  
 290 295 300  
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu  
 305 310 315 320  
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp  
 325 330 335  
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp  
 340 345 350  
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp  
 355 360 365

Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg  
 370 375 380

Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu  
 385 390 395 400

Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp  
 405 410 415

Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln  
 420 425 430

Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe  
 435 440 445

Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr  
 450 455 460

Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val  
 465 470 475 480

Phe Gly Leu Asp Asn Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp  
 485 490 495

His Pro Arg Val Val Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly  
 500 505 510

Asp

<210> 349

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXA01757

<400> 349

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gtaaaccacg tttccgtatt gtcttgagc cgaattcata atg cca aca gca agc 115  
 Met Pro Thr Ala Ser  
 1 5

cca att tat gat gtc gtt gtc gtc gga gcc ggc att tct ggc ctc atc 163  
 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile  
 10 15 20

gcc acg caa ctg ttg gac cgc gca ggt cta aac atc aaa tgc ttc gaa 211  
 Ala Thr Gln Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu  
 25 30 35

gcc tgc tca aga gtt ggc ggc cga gca gtg tct gtc caa cag tcc gat 259  
 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp  
 40 45 50

ttg ttc ctg gac ctc ggc gca aca tgg ttc tgg ctc aac gaa cca ctt 307

Leu	Phe	Leu	Asp	Leu	Gly	Ala	Thr	Trp	Phe	Trp	Leu	Asn	Glu	Pro	Leu		
55						60					65						
gtg	cag	caa	ctc	gtc	aat	aat	ctc	ggc	ctc	ggc	aca	ttc	cct	cag	gcc	355	
Val	Gln	Gln	Leu	Val	Asn	Asn	Leu	Gly	Leu	Gly	Thr	Phe	Pro	Gln	Ala	85	
70					75					80							
atc	gag	ggt	gat	gcg	ctt	ttt	gag	acg	ctt	gtc	gac	gcc	ccg	agc	cgc	403	
Ile	Glu	Gly	Asp	Ala	Leu	Phe	Glu	Thr	Leu	Val	Asp	Ala	Pro	Ser	Arg	100	
				90					95								
ctg	cgg	ggt	aac	ccc	ata	gac	gct	gct	tca	ggc	agg	ttc	caa	gca	ggg	451	
Leu	Arg	Gly	Asn	Pro	Ile	Asp	Ala	Ala	Ser	Gly	Arg	Phe	Gln	Ala	Gly	115	
			105					110									
gcc	tcc	tcg	ctt	gcg	ctc	ggg	ctt	gca	gcc	cag	ctc	aag	cca	gga	gtt	499	
Ala	Ser	Ser	Leu	Ala	Leu	Gly	Leu	Ala	Ala	Gln	Leu	Lys	Pro	Gly	Val	130	
			120				125										
tta	gaa	ctc	ggg	gac	ccc	gtc	cat	tct	ctc	agt	gag	gaa	gat	ggg	gaa	547	
Leu	Glu	Leu	Gly	Asp	Pro	Val	His	Ser	Leu	Ser	Glu	Glu	Asp	Gly	Glu	145	
	135					140											
atc	gtt	gtg	aag	tct	tcc	aaa	cag	att	gtg	agg	gca	aag	cac	gtc	atc	595	
Ile	Val	Val	Lys	Ser	Ser	Lys	Gln	Ile	Val	Arg	Ala	Lys	His	Val	Ile	165	
	150					155				160							
att	gcg	gtt	cca	ccg	gca	ctc	gct	gcc	gag	ttg	att	ggt	ttc	acc	cta	643	
Ile	Ala	Val	Pro	Pro	Ala	Leu	Ala	Ala	Glu	Leu	Ile	Gly	Phe	Thr	Leu	180	
				170					175								
gat	tta	cca	gct	gac	gtg	cga	aaa	gca	gcg	cat	cca	caa	cat	ata	gct	691	
Asp	Leu	Pro	Ala	Asp	Val	Arg	Lys	Ala	Ala	His	Pro	Gln	His	Ile	Ala	195	
			185					190									
gtg	atg	aat	tgg	gca	aag	gag	aaa	tac	acc	tta	ccc	aca	caa	gcc	gca	739	
Val	Met	Asn	Trp	Ala	Lys	Glu	Lys	Tyr	Thr	Leu	Pro	Thr	Gln	Ala	Ala	210	
		200					205										
tcg	gct	ggg	ggt	ttt	ggg	cat	gag	ctg	ttc	caa	caa	cca	ctc	gga	cat	787	
Ser	Ala	Gly	Gly	Phe	Gly	His	Glu	Leu	Phe	Gln	Gln	Pro	Leu	Gly	His	225	
	215					220											
ggg	cga	att	cat	tgg	gca	tca	acg	gaa	gtt	gcc	act	gag	ttt	ggt	gga	835	
Gly	Arg	Ile	His	Trp	Ala	Ser	Thr	Glu	Val	Ala	Thr	Glu	Phe	Gly	Gly	245	
	230				235					240							
cac	ctt	gaa	ggc	gca	gtt	cgt	gca	gga	att	cag	gct	gcg	ctt	caa	aca	883	
His	Leu	Glu	Gly	Ala	Val	Arg	Ala	Gly	Ile	Gln	Ala	Ala	Leu	Gln	Thr	260	
				250					255								
gga	ttt	aat	cta	aaa	tct	taa	ac	ctc	gt	att	ttc	cc	tg	ata		924	
Gly	Phe	Asn	Leu	Lys	Ser											265	

&lt;210&gt; 350

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350

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Met Pro Thr Ala Ser Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly
 1           5           10           15

Ile Ser Gly Leu Ile Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn
      20           25           30

Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser
      35           40           45

Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp
      50           55           60

Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly
      65           70           75           80

Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val
      85           90           95

Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly
      100          105          110

Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln
      115          120          125

Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser
      130          135          140

Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg
      145          150          155          160

Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu
      165          170          175

Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His
      180          185          190

Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu
      195          200          205

Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln
      210          215          220

Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala
      225          230          235          240

Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln
      245          250          255

Ala Ala Leu Gln Thr Gly Phe Asn Leu Lys Ser
      260          265

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&lt;210&gt; 351

&lt;211&gt; 636

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(613)



<223> RXA02159

<400> 351

[illegible]

<210> 352

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

**<400> 352**

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Thr Arg Thr	Ala Arg Gln Ala Leu	Ile Leu Gln Ile Leu	Asp Lys Gln
	20	25	30
Lys Val Thr	Ser Gln Val Gln Leu	Ser Glu Leu Leu Leu	Asp Glu Gly
	35	40	45
Ile Asp Ile	Thr Gln Ala Thr Leu	Ser Arg Asp Leu	Asp Glu Leu Gly
	50	55	60
Ala Arg Lys	Val Arg Pro Asp Gly	Gly Arg Ala Tyr Tyr	Ala Val Gly
	65	70	75
Pro Val Asp	Ser Ile Ala Arg Glu	Asp Leu Arg Gly	Pro Ser Glu Lys
	85	90	95
Leu Arg Arg	Met Leu Asp Glu Leu	Leu Val Ser Thr	Asp His Ser Gly
	100	105	110
Asn Ile Ala	Met Leu Arg Thr Pro	Pro Gly Ala Ala	Gln Tyr Leu Ala
	115	120	125
Ser Phe Ile	Asp Arg Val Gly Leu	Lys Glu Val Val	Gly Thr Ile Ala
	130	135	140
Gly Asp Asp	Thr Val Phe Val Leu	Ala Arg Asp Pro	Leu Thr Gly Lys
	145	150	155
Glu Leu Gly	Glu Leu Leu Ser Gly	Arg Thr Thr	
	165	170	

&lt;210&gt; 353

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(391)

&lt;223&gt; RXN02154

&lt;400&gt; 353

cccagaacct cggcgaagtc agcgacaagc cagtcaaggt gagcttcacc ccagtgccttg 60

caccgttacc	tcgcgaattc	tcaccactgc	aaccgcacct	ttg aaa gaa ggc gtt	115
				Leu Lys Glu Gly Val	
				1	5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa	163
Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu	
	10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca	211
Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala	
	25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa	259
Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu	
	40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307  
Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly  
55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355  
Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp  
70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401  
Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro  
90 95

ccttaaagcg gcg 414

<210> 354

**<211> 97**

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu  
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Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln  
20 25 30

Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val  
35 40 45

Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp  
50 55 60

Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu  
65 70 75 80

Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala  
85 90 95

Pro

<210> 355

<211> 1302

**<212> DNA**

<213> *Corynebacterium glutamicum*

**<220>**

<221> CDS

<222> (101) .. (1279)

<223> RXS00147

**<400> 355**

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Val Ser Lys Asp Thr  
1 5

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg	163
Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu	
10 15 20	
gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc	211
Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile	
25 30 35	
ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac	259
Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
40 45 50	
caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
105 110 115	
atg gca ggc cag ggc atc gtc ggc atc ggc gga atc gac acc cgc gca	499
Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc	595
Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
150 155 160 165	
aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct	643
Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc	691
Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu  
 250 255 260

gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931  
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln  
 265 270 275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979  
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly  
 280 285 290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc  
 1027

His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile  
 295 300 305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc  
 1075

Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly  
 310 315 320 325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc  
 1123

Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys  
 330 335 340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca  
 1171

Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala  
 345 350 355

tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca  
 1219

Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala  
 360 365 370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag  
 1267

Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln  
 375 380 385

aag aaa ggc gca taaataacat gccaaagcgt tca  
 1302

Lys Lys Gly Ala  
 390

&lt;210&gt; 356

&lt;211&gt; 393

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser  
 1 5 10 15

Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe  
 20 25 30

Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr  
 35 40 45

Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg  
 50 55 60  
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn  
 65 70 75 80  
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu  
 85 90 95  
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr  
 100 105 110  
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly  
 115 120 125  
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile  
 130 135 140  
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu  
 145 150 155 160  
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu  
 165 170 175  
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly  
 180 185 190  
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn  
 195 200 205  
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro  
 210 215 220  
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val  
 225 230 235 240  
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val  
 245 250 255  
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile  
 260 265 270  
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr  
 275 280 285  
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His  
 290 295 300  
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu  
 305 310 315 320  
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile  
 325 330 335  
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu  
 340 345 350  
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala  
 355 360 365

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met  
 370 375 380

Asp Ala Asp Ala Gln Lys Lys Gly Ala  
 385 390

<210> 357

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXS00905

<400> 357

cgctgccctt ctatgctgct cctagttacc cctgcacaaa tagcggtttt tctcagcat 60

tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115  
 Met Thr Gln Phe Glu  
 1 5

aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163  
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile  
 10 15 20

ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211  
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp  
 25 30 35

cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259  
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu  
 40 45 50

aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307  
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp  
 55 60 65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355  
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro  
 70 75 80 85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403  
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu  
 90 95 100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451  
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly  
 105 110 115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499  
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn  
 120 125 130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547  
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp  
 135 140 145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595

Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly  
 150 155 160 165  
 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643  
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp  
 170 175 180  
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691  
 Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr  
 185 190 195  
 cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739  
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr  
 200 205 210  
 gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787  
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala  
 215 220 225  
 gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835  
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg  
 230 235 240 245  
 gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883  
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys  
 250 255 260  
 ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924  
 Leu Glu Gly Arg Ala Leu  
 265

&lt;210&gt; 358

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn  
 1 5 10 15  
 Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn  
 20 25 30  
 Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys  
 35 40 45  
 Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu  
 50 55 60  
 Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly  
 65 70 75 80  
 Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val  
 85 90 95  
 Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr  
 100 105 110  
 Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala  
 115 120 125



Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val  
 130 135 140

Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly  
 145 150 155 160

Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys  
 165 170 175

Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn  
 180 185 190

Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly  
 195 200 205

Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly  
 210 215 220

Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val  
 225 230 235 240

Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys  
 245 250 255

Gln His His Arg Lys Leu Glu Gly Arg Ala Leu  
 260 265

<210> 359

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXS00906

<400> 359

accgtggaca cccttgaagg cgctgttcac tccggccaga acggtggcgc tgccccagat 60

gctgttgctg ctctcgtgcg cgttctggat actttgcgcg atg aac acg gac gca 115  
 Met Asn Thr Asp Ala  
 1 5

ccg tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct 163  
 Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro  
 10 15 20

tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211  
 Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val  
 25 30 35

gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259  
 Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg  
 40 45 50

cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca 307  
 Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala  
 55 60 65

ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355  
 Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val 85  
 70 75 80

cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403  
 Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His 100  
 90 95

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451  
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp 115  
 105 110

gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499  
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser 130  
 120 125

acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547  
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val 145  
 135 140

acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595  
 Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu 165  
 150 155 160

gtc aac cca taagcagaat tggcactcta cgg 627  
 Val Asn Pro

&lt;210&gt; 360

&lt;211&gt; 168

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 360

Met Asn Thr Asp Ala Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn  
 1 5 10 15

Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly  
 20 25 30

Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser  
 35 40 45

Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr  
 50 55 60

Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys  
 65 70 75 80

Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu  
 85 90 95

Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile  
 100 105 110

Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr  
 115 120 125

Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

130		135		140	
Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys					
145		150		155	160
Thr Glu Leu Ile Glu Val Asn Pro					
		165			

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<210> 361
<211> 246
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(223)  
<223> RXS00907
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<400> 361
cctgagcgcgt gcgtacgagg gcaaggatct tgtcaccgaa ggcagcggcg gatccattcc 60

actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115
Leu Ala Leu Tyr Gly
1 5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163
Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp
10 15 20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211
Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu
25 30 35

aac tac acc aag tagaccçaaa agcaggcggtt aac 246
Asn Tyr Thr Lys
40

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<210> 362
<211> 41
<212> PRT
<213> Corynebacterium glutamicum
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<400> 362
Leu Ala Leu Tyr Gly Val Glu Glu Pro Leu Thr Val Ile His Ser Ala
  1             5             10             15
Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu
      20             25             30
Ala Leu Phe Leu Leu Asn Tyr Thr Lys
    35             40

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<210> 363
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum
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**<220>**

<221> CDS  
 <222> (101)..(1258)  
 <223> RXS02001

<400> 363

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cgcggtttcgt catggataag gactgtgttc gggaccattg cgatactcgt gtcaaaaggc 60

gatagtccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115
                                         Met Pro Val Ile Asn
                                         1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163
Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu
                        10                        15                        20

cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe
                        25                        30                        35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly
                        40                        45                        50

atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly
                        55                        60                        65

ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu
                        70                        75                        80                        85

att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403
Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala
                        90                        95                        100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr
                        105                        110                        115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln
                        120                        125                        130

cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547
Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly
                        135                        140                        145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln
                        150                        155                        160                        165

ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met
                        170                        175                        180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His
                        185                        190                        195

ggg gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly

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200	205	210	
att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc I1 Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val 215 220 225			787
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp 230 235 240 245			835
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe 250 255 260			883
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val 265 270 275			931
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn 280 285 290			979
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct 1027 Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala 295 300 305			
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg 1075 Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser 310 315 320 325			
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg 1123 Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro 330 335 340			
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac 1171 Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn 345 350 355			
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc 1219 Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe 360 365 370			
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg 1268 Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly 375 380 385			
cgctcgaaga tgc 1281			
<210> 364			
<211> 386			
<212> PRT			
<213> Corynebacterium glutamicum			

&lt;400&gt; 364

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Met Pro Val Ile Asn Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg
 1           5           10           15

Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val
          20           25           30

Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp
          35           40           45

Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His
          50           55           60

Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala
          65           70           75           80

Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro
          85           90           95

Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu
          100          105          110

Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val
          115          120          125

Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val
          130          135          140

Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr
          145          150          155          160

Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr
          165          170          175

Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr
          180          185          190

Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile
          195          200          205

Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg
          210          215          220

Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His
          225          230          235          240

Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly
          245          250          255

Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg
          260          265          270

Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala
          275          280          285

Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala
          290          295          300

Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val
          305          310          315          320

```



cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat 499  
 His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp  
 120 125 130

gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca 547  
 Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro  
 135 140 145

tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta 595  
 Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu  
 150 155 160 165

gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc 643  
 Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val  
 170 175 180

ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct 691  
 Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala  
 185 190 195

gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt 739  
 Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly  
 200 205 210

tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att 787  
 Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile  
 215 220 225

gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat 835  
 Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp  
 230 235 240 245

ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac 883  
 Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn  
 250 255 260

acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac 931  
 Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn  
 265 270 275

gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt 979  
 Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg  
 280 285 290

ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac  
 1027  
 Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr  
 295 300 305

ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act  
 1075  
 Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr  
 310 315 320 325

gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct  
 1123  
 Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala  
 330 335 340

tac cgg tgg act gcg tcg gag gat ttc ccc tcc att cct aag gca ttc  
 1171



Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe  
345 350 355

aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag  
1219

Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln  
360 365 370

tgg aca gaa gcc gta gaa aga gac cgc gtg gca tcg gat gtg cca gcc  
1267

Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala  
375 380 385

aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct  
1315

Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala  
390 395 400 405

gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac  
1363

Ala Thr Arg Ala Ala Ala Ala Ala Leu Leu Thr Tyr Leu Gly Thr Asn  
410 415 420

taatcatcta gttttctgcg acg  
1386

<210> 366

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

Met Ser Arg Ile Ser Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser  
1 5 10 15

Trp Gln Glu Ala Ala Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser  
20 25 30

Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg  
35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala  
50 55 60

Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met  
65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro  
85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val  
100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala  
115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile  
130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met

145	150	155	160
Val Ala Gly Gly	Leu Val Asp Leu Ile	Pro Arg Pro Asp Val	Cys Phe
	165	170	175
Gly Gln His Val	Val Pro Gly Ala Ala	Gly Thr Val Met	Ser Met Pro
	180	185	190
Gly Gly Ala Leu	Ala Ala Cys Asp	Ser Ile Glu Ile	Arg Ile Gln Gly
	195	200	205
Arg Ser Ala His	Gly Ser Met Pro	His Asn Ser Ile	Asp Pro Thr Tyr
	210	215	220
Val Ala Ala Met	Ile Val Val Arg	Leu Gln Gly Ile	Val Gly Arg Glu
	225	230	235
Val Ser Pro Glu	Asp Phe Ala Val	Ile Ser Val Gly	Thr Leu Gln Ser
	245	250	255
Gly Asn Thr Asn	Asn Thr Ile Pro	Ala Ser Ala Arg	Leu Val Leu Asn
	260	265	270
Cys Arg Phe Tyr	Asn Asp Lys Val	Lys His Lys Val	Tyr Arg Ala Ile
	275	280	285
Glu Arg Val Val	Arg Gly Glu Cys	Leu Ala Ser Gly	Ile Glu Glu Glu
	290	295	300
Pro Val Ile Glu	Tyr Phe Ala His	Gly Asp Leu Thr	Asn Asn Thr Pro
	305	310	315
Val Val Phe Asp	Thr Val Arg Pro	Val Phe Asp Asp	Val Phe Gly Glu
	325	330	335
Asp Ser Ile Asp	Ala Tyr Arg Trp	Thr Ala Ser Glu	Asp Phe Pro Ser
	340	345	350
Ile Pro Lys Ala	Phe Asn Ser Pro	Tyr Leu Tyr Trp	Thr Ile Gly Val
	355	360	365
Thr Pro Arg Asp	Gln Trp Thr Glu	Ala Val Glu Arg	Asp Arg Val Ala
	370	375	380
Ser Asp Val Pro	Ala Asn His Met	Gly Asp Phe Leu	Pro Asp Tyr Ala
	385	390	395
Pro Thr Met Ser	Ala Ala Thr Arg	Ala Ala Ala Ala	Leu Leu Thr
	405	410	415
Tyr Leu Gly Thr	Asn		
	420		

&lt;210&gt; 367

&lt;211&gt; 3462

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(3439)

&lt;223&gt; RXS02234

&lt;400&gt; 367

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tgatggatgc	agacgctcag	aagaaaggcg	cataaataac	atg	cca	aag	cgt	tca	115
				Met	Pro	Lys	Arg	Ser	
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gat	att	aac	cac	gtc	ctc	gtc	atc	ggg	tcc	ggc	ccc	atc	gtc	att	ggc	163
Asp	Ile	Asn	His	Val	Leu	Val	Ile	Gly	Ser	Gly	Pro	Ile	Val	Ile	Gly	
			10					15						20		

cag	gca	tgt	gaa	ttc	gac	tac	tcc	ggc	acc	cag	gct	tgc	cgc	gtg	ctg	211
Gln	Ala	Cys	Glu	Phe	Asp	Tyr	Ser	Gly	Thr	Gln	Ala	Cys	Arg	Val	Leu	
			25					30					35			

aag	gaa	gag	gga	ctg	cgc	gtc	acc	ctc	atc	aac	tcc	aac	cca	gca	acg	259
Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn	Ser	Asn	Pro	Ala	Thr	
			40				45					50				

atc	atg	acc	gac	cca	gaa	atg	gct	gac	cac	acc	tac	gtg	gag	cca	atc	307
Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr	Tyr	Val	Glu	Pro	Ile	
	55					60					65					

gag	ccg	gaa	tac	atc	gac	aag	att	ttc	gct	aag	gaa	atc	gag	cag	ggc	355
Glu	Pro	Glu	Tyr	Ile	Asp	Lys	Ile	Phe	Ala	Lys	Glu	Ile	Glu	Gln	Gly	
	70				75					80					85	

cac	cca	atc	gac	gcc	gtc	ctg	gca	acc	ctt	ggg	ggc	cag	act	gca	ctt	403
His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly	Gly	Gln	Thr	Ala	Leu	
				90				95						100		

aac	gca	gct	atc	cag	ctg	gat	cgc	ctc	ggc	atc	ctg	gaa	aag	tac	ggc	451
Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile	Leu	Glu	Lys	Tyr	Gly	
			105				110						115			

gtt	gaa	ctc	atc	ggg	gca	gac	atc	gat	gcc	att	gag	cgc	ggc	gaa	gat	499
Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile	Glu	Arg	Gly	Glu	Asp	
		120					125					130				

cgc	cag	aag	ttc	aag	gat	att	gtc	acc	acc	atc	ggg	ggc	gaa	tcc	gcg	547
Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile	Gly	Gly	Glu	Ser	Ala	
	135				140					145						

cgt	tcc	cgc	gtc	tgc	cac	aac	atg	gaa	gaa	gtc	cac	gag	act	gtc	gca	595
Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	Val	His	Glu	Thr	Val	Ala	
	150				155					160					165	

gaa	ctc	ggc	ctt	cca	gta	gtc	gtg	cgt	cca	tcc	ttc	act	atg	ggg	ggc	643
Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser	Phe	Thr	Met	Gly	Gly	
				170				175						180		

ctg	ggc	tcc	ggg	ctt	gca	tac	aac	acc	gaa	gac	ctt	gag	cgc	atc	gct	691
Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	Asp	Leu	Glu	Arg	Ile	Ala	
			185				190						195			

ggg	ggc	gga	ctt	gct	gca	tct	cct	gaa	gca	aac	gtc	ttg	atc	gaa	gaa	739
Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	Asn	Val	Leu	Ile	Glu	Glu	
		200					205					210				

tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc	787
Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr	
215 220 225	
gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg	835
Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu	
230 235 240 245	
ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg	883
Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu	
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act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc	931
Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile	
265 270 275	
cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc	979
Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile	
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Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val	
295 300 305	
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1075	
Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala	
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1123	
Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr	
330 335 340	
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1171	
Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp	
345 350 355	
tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc	
1219	
Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly	
360 365 370	
gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg	
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Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met	
375 380 385	
tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc	
1315	
Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser	
390 395 400 405	
ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc	
1363	
Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe	
410 415 420	

gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag  
 1411  
 Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys  
 425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt  
 1459  
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu  
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 Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp  
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 Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val  
 470 475 480 485

gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg  
 1603  
 Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met  
 490 495 500

ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc  
 1651  
 Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly  
 505 510 515

gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta  
 1699  
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val  
 520 525 530

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 1747  
 Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro  
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tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc  
 1795  
 Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val  
 550 555 560 565

gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca  
 1843  
 Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro  
 570 575 580

aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca  
 1891  
 Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala  
 585 590 595

gct ctt gag ctc tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc  
 1939  
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys  
 600 605 610

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac  
1987

Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr  
615 620 625

ttc gag cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag  
2035

Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu  
630 635 640 645

gcg cag tcc ggc acc gtc gca ggt gtt atc gtc cag ctt ggt ggc cag  
2083

Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln  
650 655 660

act cct ctg ggc ttg gca gat cgt ttg aag aag gct ggc gtc cct gtc  
2131

Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val  
665 670 675

att ggt acc tcc cca gag gca atc gac atg gct gag gac cgt ggc gag  
2179

Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu  
680 685 690

ttc ggt gca ctg ctg aac cgc gag cag ctt cct gct cca gca ttc ggc  
2227

Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly  
695 700 705

acc gca acc tct ttc gaa gag gct cgc aca gta gcc gat gag atc agc  
2275

Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser  
710 715 720 725

tac cca gtg ctg gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg  
2323

Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met  
730 735 740

gag att gtc tac gat gag gct tcc ctc gag gat tac atc aac cgc gca  
2371

Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala  
745 750 755

act gag ttg tct tct gac cac cca gtg ctg gtt gac cgc ttc cta gac  
2419

Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp  
760 765 770

aac gct att gag atc gac gtc gac gca ctg tgc gac ggc gac gag gtc  
2467

Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val  
775 780 785

tac ctg gca ggc gtc atg gag cac atc gag gaa gcc ggc att cac tcc  
2515

Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser  
790 795 800 805

ggt gac tcc gca tgt gca ctt cct cca atg act ttg ggc gca cag gac  
2563

Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp  
810 815 820

atc gag aag gtc cgc gaa gca acc aag aag ctg gct ctg ggc atc ggt  
2611

Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly  
825 830 835

gta cag ggc ctg atg aac gtc cag tac gca ctc aag gac gac atc ctc  
2659

Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu  
840 845 850

tac gtc atc gag gca aac cca cgt gca tcc cgc acc gtg ccg ttc gtc  
2707

Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg Thr Val Pro Phe Val  
855 860 865

tcc aag gca acg ggc gtc aac ctg gcc aag gca gca tcc cgt atc gca  
2755

Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala  
870 875 880 885

gtg ggc gcc acc atc aag gat ctc caa gat gag ggc atg att cct acc  
2803

Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu Gly Met Ile Pro Thr  
890 895 900

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2851

Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys  
905 910 915

gaa gca gtg ttg ccg ttc aac cgc ttc cgt cgc cca gat gga aag acc  
2899

Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr  
920 925 930

ctg gac acc ctg ctt tcc cca gag atg aag tcc act ggc gag gtc atg  
2947

Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met  
935 940 945

ggc ttg gcc aac aac ttc ggc gct gca tat gca aag gct gaa gct ggc  
2995

Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly  
950 955 960 965

gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct  
3043

Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala  
970 975 980

aac cgc gac aag cgc acc ctg atc ctg cca atc cag cgc ctg gcg ttg  
3091

Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu  
985 990 995

atg ggc tac aag atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc  
3139

Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg  
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cgc aac ggc att gag tgt gaa gtt gtg ctc aag gct tcc gac atc cgc  
3187

Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg  
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gaa ggt gta gag ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa  
3235

Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu  
1030 1035 1040 1045

gtt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac  
3283

Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His  
1050 1055 1060

gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg  
3331

Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu  
1065 1070 1075

atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc  
3379

Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala  
1080 1085 1090

ctg cgt gag ggc gtt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac  
3427

Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His  
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3462

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1110

<210> 368

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 368

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Ala Cys Arg Val Leu Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn  
35 40 45

Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr  
50 55 60

Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys  
65 70 75 80



Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly  
                             85                            90                            95  
 Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile  
                             100                            105                            110  
 Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile  
                             115                            120                            125  
 Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile  
                             130                            135                            140  
 Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu Val  
                             145                            150                            155                            160  
 His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser  
                             165                            170                            175  
 Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp  
                             180                            185                            190  
 Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn  
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 Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu  
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 Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala  
                             245                            250                            255  
 Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln  
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 Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn  
                             275                            280                            285  
 Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu  
                             290                            295                            300  
 Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr  
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 Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr  
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 Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe  
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 Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser  
                             370                            375                            380  
 Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn  
                             385                            390                            395                            400

Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys  
 405 410 415  
 Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val  
 420 425 430  
 Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu  
 435 440 445  
 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser  
 450 455 460  
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe  
 465 470 475 480  
 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg  
 485 490 495  
 Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg  
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 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu  
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 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe  
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 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala  
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 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile  
 565 570 575  
 Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr  
 580 585 590  
 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr  
 595 600 605  
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr  
 610 615 620  
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu  
 625 630 635 640  
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val  
 645 650 655  
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys  
 660 665 670  
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala  
 675 680 685  
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro  
 690 695 700  
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val  
 705 710 715 720  
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu

725					730					735					
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			740					745					750		
Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu	Val
		755					760					765			
Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu	Cys
	770					775					780				
Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu	Glu
785					790					795					800
Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met	Thr
				805					810					815	
Leu	Gly	Ala	Gln	Asp	Ile	Glu	Lys	Val	Arg	Glu	Ala	Thr	Lys	Lys	Leu
			820					825					830		
Ala	Leu	Gly	Ile	Gly	Val	Gln	Gly	Leu	Met	Asn	Val	Gln	Tyr	Ala	Leu
		835					840					845			
Lys	Asp	Asp	Ile	Leu	Tyr	Val	Ile	Glu	Ala	Asn	Pro	Arg	Ala	Ser	Arg
	850					855					860				
Thr	Val	Pro	Phe	Val	Ser	Lys	Ala	Thr	Gly	Val	Asn	Leu	Ala	Lys	Ala
865					870					875					880
Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	Glu
				885					890					895	
Gly	Met	Ile	Pro	Thr	Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp	Ala
			900					905					910		
Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	Arg
		915					920					925			
Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys	Ser
	930					935					940				
Thr	Gly	Glu	Val	Met	Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr	Ala
945					950					955					960
Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	Val
				965					970					975	
Phe	Val	Thr	Val	Ala	Asn	Arg	Asp	Lys	Arg	Thr	Leu	Ile	Leu	Pro	Ile
			980					985					990		
Gln	Arg	Leu	Ala	Leu	Met	Gly	Tyr	Lys	Ile	Leu	Ala	Thr	Glu	Gly	Thr
		995					1000					1005			
Ala	Gly	Met	Leu	Arg	Arg	Asn	Gly	Ile	Glu	Cys	Glu	Val	Val	Leu	Lys
	1010					1015					1020				
Ala	Ser	Asp	Ile	Arg	Glu	Gly	Val	Glu	Gly	Lys	Ser	Ile	Val	Asp	Arg
1025					1030					1035					1040
Ile	Arg	Glu	Gly	Glu	Val	Asp	Leu	Ile	Leu	Asn	Thr	Pro	Ala	Gly	Ser
			1045						1050					1055	

Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr  
 1060 1065 1070

Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val  
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Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu  
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<210> 369

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(3198)

<223> FRXA02234

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 Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala  
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aag gaa atc gag cag ggc cac cca atc gac gcc gtc ctg gca acc ctt 144  
 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu  
 35 40 45

ggt ggc cag act gca ctt aac gca gct atc cag ctg gat cgc ctc ggc 192  
 Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly  
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atc ctg gaa aag tac ggc gtt gaa ctc atc ggt gca gac atc gat gcc 240  
 Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala  
 65 70 75 80

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 Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr  
 85 90 95

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 Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu  
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gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca 384  
 Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro  
 115 120 125

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 Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu  
 130 135 140

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Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu	
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Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile	
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Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val	
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Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile	
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Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala	
260 265 270	
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Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr	
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 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala  
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 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln  
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2256																				
Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu					
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gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg																				
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2400

Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala  
785 790 795 800

ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc  
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Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser  
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cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag  
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Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys  
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gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat  
2544

Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp  
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2592

Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp  
850 855 860

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Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg  
865 870 875 880

cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag  
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Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys  
885 890 895

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Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr  
900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc  
2784

Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr  
915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca  
2832

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro  
930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc  
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Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly  
945 950 955 960



acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc  
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 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu  
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aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat  
 2976  
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp  
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cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt  
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 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly  
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tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg  
 3072  
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val  
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 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala  
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 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu  
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 Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly  
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 Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala  
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 Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr

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Asp	Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala				
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Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile				
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Glu	Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val				
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Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala				
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Phe	Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala				
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Lys	Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala				
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 485 490 495  
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 Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val  
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 690 695 700  
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Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu  
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 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met  
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 995 1000 1005  
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gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547  
 Ala Lys Trp Leu Ser Glu His Gln Asn Leu Phe Ser Trp Lys Asn  
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 150 155 160 165

gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643

Asp	Ala	Val	Val	Ile	Asn	Val	Gly	Glu	Lys	Gly	Ala	Ala	Gln	Arg	Arg		
				170					175					180			
att	cac	gtc	aat	ggc	gat	gct	ggg	cat	ggg	tcc	att	cct	ttc	gac	cgt	691	
Ile	His	Val	Asn	Gly	Asp	Ala	Gly	His	Gly	Ser	Ile	Pro	Phe	Asp	Arg		
			185					190					195				
gac	agc	gct	att	gtc	aag	atc	ggg	gaa	gtc	gcc	cgc	cga	atc	gct	gcc	739	
Asp	Ser	Ala	Ile	Val	Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala		
		200					205					210					
gcc	gat	ctg	aag	gta	gcc	aag	gac	gat	atc	tgg	caa	ggc	ttc	gtc	caa	787	
Ala	Asp	Leu	Lys	Val	Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln		
	215					220					225						
gcg	cac	cgt	ttc	gac	cca	gaa	acg	gag	cag	gcg	ctt	ctt	agc	ggg	acc	835	
Ala	His	Arg	Phe	Asp	Pro	Glu	Thr	Glu	Gln	Ala	Leu	Leu	Ser	Gly	Thr		
230					235				240						245		
tcc	cct	gag	gcc	tac	gca	gag	ttc	ggc	gga	ctc	tcc	cgc	ttc	gcc	cac	883	
Ser	Pro	Glu	Ala	Tyr	Ala	Glu	Phe	Gly	Gly	Leu	Ser	Arg	Phe	Ala	His		
				250				255						260			
gcg	gtg	tct	cat	ctc	acg	atc	gcc	caa	act	gtg	gtt	cgt	gca	ggg	caa	931	
Ala	Val	Ser	His	Leu	Thr	Ile	Ala	Gln	Thr	Val	Val	Arg	Ala	Gly	Gln		
			265				270						275				
gcc	atc	aat	gta	ttg	cca	tcg	cat	gcg	tac	ttg	gaa	ctg	gat	atc	cgt	979	
Ala	Ile	Asn	Val	Leu	Pro	Ser	His	Ala	Tyr	Leu	Glu	Leu	Asp	Ile	Arg		
		280					285					290					
acc	ctt	cca	ggc	caa	acc	aat	gac	tat	gtt	gat	gac	acc	ctg	cgt	gct		
1027																	
Thr	Leu	Pro	Gly	Gln	Thr	Asn	Asp	Tyr	Val	Asp	Asp	Thr	Leu	Arg	Ala		
	295					300					305						
gct	ctg	ggc	gat	ctt	gcc	gat	gaa	gta	gaa	atc	gaa	cac	ctc	atc	tct		
1075																	
Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile	Ser		
310					315				320					325			
gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	ttg		
1123																	
Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr	Leu		
				330				335						340			
gaa	aaa	gtt	ctt	ggg	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	att		
1171																	
Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro	Ile		
			345					350					355				
att	tcc	tct	ggg	ggc	tct	gac	ctg	cgc	ttt	ggg	cgt	cga	cta	ggc	ggg		
1219																	
Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly	Gly		
			360				365					370					
gtt	ggg	tat	ggg	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	gaa		
1267																	
Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala	Glu		
	375					380					385						

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat  
1315

Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp  
390 395 400 405

ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta  
1363

Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu  
410 415 420

ggc taaaaacatg aagcaggagt ctt

1389

Gly

<210> 372

<211> 422

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 372

Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu  
1 5 10 15

Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys  
20 25 30

Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly  
35 40 45

Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val  
50 55 60

Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu  
65 70 75 80

Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe  
85 90 95

Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly  
100 105 110

Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala  
115 120 125

Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu  
130 135 140

Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro  
145 150 155 160

Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly  
165 170 175

Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser  
180 185 190

Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala  
195 200 205

Arg Arg Il Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp  
 210 215 220  
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala  
 225 230 235 240  
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu  
 245 250 255  
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val  
 260 265 270  
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu  
 275 280 285  
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp  
 290 295 300  
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile  
 305 310 315 320  
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg  
 325 330 335  
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala  
 340 345 350  
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly  
 355 360 365  
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu  
 370 375 380  
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala  
 385 390 395 400  
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val  
 405 410 415  
 Val Arg Glu Phe Leu Gly  
 420

&lt;210&gt; 373

&lt;211&gt; 525

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(502)

&lt;223&gt; RXS02937

&lt;400&gt; 373

gctaccgcga agaactgtac tagttcttcc atcagcaccc gcagttgtct ttgcaagagt 60

tcgaaacatc caacgcattg gtgacaccgg tggtgtcgcg gtg atc agc aat ggg 115  
 Val Ile Ser Asn Gly  
 1 5

gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163



Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met  
                                   10                                  15                                  20  
 gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211  
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val  
                                   25                                  30                                  35  
 gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259  
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His  
                                   40                                  45                                  50  
 gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307  
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser  
                                   55                                  60                                  65  
 cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355  
 His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala  
                                   70                                  75                                  80                                  85  
 gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403  
 Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala  
                                   90                                  95                                  100  
 ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451  
 Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu  
                                   105                                  110                                  115  
 gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499  
 Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val  
                                   120                                  125                                  130  
 aaa taattggcta atgaatcctt ttc 525  
 Lys

<210> 374  
 <211> 134  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 374  
 Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile  
   1                                  5                                  10                                  15  
 Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr  
                                   20                                  25                                  30  
 Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala  
                                   35                                  40                                  45  
 His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val  
                                   50                                  55                                  60  
 Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala  
                                   65                                  70                                  75                                  80  
 Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala  
                                   85                                  90                                  95  
 Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp

100	105	110	
Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala			
115	120	125	
Ser Ala Trp Leu Val Lys			
130			
<210> 375			
<211> 966			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(943)			
<223> RXA02194			
<400> 375			
gaaatctccc agctcattta ttggaccag gtcacatgg ttgctcgcg cctgaagcca 60			
gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115			
		Met Leu Lys Ile Ala	
		1 5	
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163			
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala			
	10	15	20
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211			
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe			
	25	30	35
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259			
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile			
	40	45	50
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307			
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg			
	55	60	65
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355			
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu			
	70	75	80
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403			
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu			
	90	95	100
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451			
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro			
	105	110	115
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499			
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val			
	120	125	130
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547			
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala			
	135	140	145

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595  
Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln  
150 155 160 165  
  
ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643  
Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile  
170 175 180  
  
gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691  
Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu  
185 190 195  
  
cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739  
Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp  
200 205 210  
  
tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787  
Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro  
215 220 225  
  
ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835  
Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val  
230 235 240 245  
  
gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883  
Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp  
250 255 260  
  
aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931  
Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg  
265 270 275  
  
atc gcc cgc atc tagttttaac taccctcgaa aat 966  
Ile Ala Arg Ile  
280

&lt;210&gt; 376

&lt;211&gt; 281

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala  
1 5 10 15  
  
Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys  
20 25 30  
  
Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu  
35 40 45  
  
Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu  
50 55 60  
  
Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His  
65 70 75 80  
  
Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala  
85 90 95

Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile  
 100 105 110

Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly  
 115 120 125

Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile  
 130 135 140

Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg  
 145 150 155 160

Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr  
 165 170 175

Ser Glu Ala Val Ile Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu  
 180 185 190

Gln Gln Ile Leu Leu Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn  
 195 200 205

Phe Leu Met Leu Asp Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala  
 210 215 220

Thr Ala Val Thr Pro Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala  
 225 230 235 240

Arg Asp Asn Trp Val Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala  
 245 250 255

Asn Ala Ile Met Asp Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu  
 260 265 270

Ala Ser Glu Ile Arg Ile Ala Arg Ile  
 275 280

&lt;210&gt; 377

&lt;211&gt; 393

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(370)

&lt;223&gt; RXA02195

&lt;400&gt; 377

tcgagccggc aggtgtcgca aaataaaacc aggtggggga gtgaaattat tcgactaata 60

tcctccccc aacacacatt gataactgtt gtgtggaaga atg tac cga gtg aag 115  
 Met Tyr Arg Val Lys  
 1 5

aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc 163  
 Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg  
 10 15 20

cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat 211  
 Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

```

                25                30                35
cta ggt aag aag gtc atc gaa gaa gcc gga gag gtc tgg att gca gcc 259
Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu Val Trp Ile Ala Ala
      40                45                50

gag tat gag acc gat gaa gag cta gcc gga gaa atc tcc cag ctc att 307
Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu Ile Ser Gln Leu Ile
      55                60                65

tat tgg acc cag gtc atc atg gtt gct cgc ggc ctg aag cca gaa gat 355
Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly Leu Lys Pro Glu Asp
      70                75                80                85

atc tac aag aac ctg taggagtttt aaagcaatca tgt 393
Ile Tyr Lys Asn Leu
      90

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&lt;210&gt; 378

&lt;211&gt; 90

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 378

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Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn
 1                5                10                15

Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp
      20                25                30

Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu
      35                40                45

Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu
      50                55                60

Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly
      65                70                75                80

Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu
      85                90

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&lt;210&gt; 379

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(454)

&lt;223&gt; RXA01097

&lt;400&gt; 379

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gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag 60

taaaggggagc cattaaagat gcaggatttg aggtgcgga atg agt gac aat cca 115
      Met Ser Asp Asn Pro
      1                5

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caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163  
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn  
                     10                    15                    20  
  
 gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211  
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu  
                     25                    30                    35  
  
 gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259  
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu  
                     40                    45                    50  
  
 gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307  
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp  
                     55                    60                    65  
  
 atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355  
 Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala  
                     70                    75                    80                    85  
  
 ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403  
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly  
                     90                    95                    100  
  
 ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451  
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu  
                     105                    110                    115  
  
 ctg taaaagcaac aacgattaag gaa 477  
 Leu

&lt;210&gt; 380

&lt;211&gt; 118

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys  
           1                    5                    10                    15  
  
 Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala  
                     20                    25                    30  
  
 Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala  
                     35                    40                    45  
  
 Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser  
                     50                    55                    60  
  
 Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu  
                     65                    70                    75                    80  
  
 Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr  
                     85                    90                    95  
  
 Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe  
                     100                    105                    110  
  
 Asp Asn Asp Val Leu Leu

115

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<210> 381
<211> 861
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(838)  
<223> RXA01100
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<400> 381																
gctgtgtgggct actcaattcc acccagaaaa atcaggtgac gcaggcgcac agctactgcg 60																
aaactggatc aactacatct aacagatagg atcaatattc atg acc ttc act att 115																
Met Thr Phe Thr Ile 5																
1																
ctt cct gca gtc gat gta gtt aac gga caa gca gtt cgc cta gat cag 163																
Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala Val Arg Leu Asp Gln 20																
10 15																
ggc gag gcc ggc act gaa aag tct tat ggc acc cct ttg gaa tcc gca 211																
Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr Pro Leu Glu Ser Ala 35																
25 30																
ctg aag tgg cag gag cag ggt gca aag tgg ttg cac ttt gtg gac ctg 259																
Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu His Phe Val Asp Leu 50																
40 45																
gac gca gcg ttc aac cgt ggt tcc aac cat gag atg atg gcg gaa att 307																
Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu Met Met Ala Glu Ile 65																
55 60																
gtc ggc aag ctc gat gtt gat gtg gag ctc act ggc ggt atc cgt gat 355																
Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr Gly Gly Ile Arg Asp 85																
70 75 80																
gat gag tct ctg gag cgc gcg ctg gca acc ggt gca cgt cgt gta aac 403																
Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly Ala Arg Arg Val Asn 100																
90 95																
att ggt acc gct gct ctg gag aag cca gag tgg att gct tct gcg att 451																
Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp Ile Ala Ser Ala Ile 115																
105 110																
caa cgc tat ggc gag aag att gct gtc gat atc gct gtg cgt ttg gaa 499																
Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile Ala Val Arg Leu Glu 130																
120 125 130																
gat ggt gaa tgg cgc acc cgt gga aac ggt tgg gtc tcc gat ggt ggc 547																
Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp Val Ser Asp Gly Gly 145																
135 140																
gat ctg tgg gaa gtt ctc gag cgt ttg gat tcc caa ggt tgt gca cgt 595																
Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser Gln Gly Cys Ala Arg 165																
150 155 160																
ttc gtg gtt acc gat gtg tcc aag gac ggc acc ttg agt ggt cca aat 643																

Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn  
                             170                            175                            180  
  
 gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691  
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val  
                             185                            190                            195  
  
 gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739  
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys  
                             200                            205                            210  
  
 tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787  
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr  
                             215                            220                            225  
  
 gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835  
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu  
                             230                            235                            240                            245  
  
 ggt taatacatgg atgctcgtgg gat 861  
 Gly

&lt;210&gt; 382

&lt;211&gt; 246

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala  
           1                            5                            10                            15  
  
 Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr  
                             20                            25                            30  
  
 Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu  
                             35                            40                            45  
  
 His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu  
           50                            55                            60  
  
 Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr  
           65                            70                            75                            80  
  
 Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly  
                             85                            90                            95  
  
 Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp  
                             100                            105                            110  
  
 Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile  
           115                            120                            125  
  
 Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp  
           130                            135                            140  
  
 Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser  
           145                            150                            155                            160  
  
 Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr



	165		170		175
Leu Ser Gly Pro Asn Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr	180		185		190
Asp Ala Pro Ile Val Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val	195		200		205
Leu Glu Leu Ala Lys Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile	210		215		220
Gly Lys Ala Leu Tyr Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala	225		230		235
Ala Val Glu Lys Leu Gly	245				

&lt;210&gt; 383

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(733)

&lt;223&gt; RXA01101

&lt;400&gt; 383

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atcgcagcta ggccagtgtg gtggatataa aacccttttg gggagaaaga aactcgactg 60
cggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115
                                     Met Thr Lys Thr Val 5
                                     1
gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163
Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala 20
                                     10
cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211
Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val 35
                                     25
tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259
Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp 50
                                     40
gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307
Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly 65
                                     55
cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355
Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met 85
                                     70
cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403
Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly 100
                                     90
tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451
Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu

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105	110	115	
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg			499
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met			
120	125	130	
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat			547
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr			
135	140	145	
ggg gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca			595
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro			
150	155	160	165
gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg			643
Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val			
170	175	180	
gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt			691
Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly			
185	190	195	
gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc			733
Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile			
200	205	210	
taacagatag gatcaatatt cat			756

&lt;210&gt; 384

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 384

Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg		
1	5	10
Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser		
20	25	30
Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly		
35	40	45
Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly		
50	55	60
His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly		
65	70	75
Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly		
85	90	95
Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu		
100	105	110
Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro		
115	120	125
Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr		
130	135	140

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp  
 145 150 155 160  
 Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg  
 165 170 175  
 Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His  
 180 185 190  
 Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile  
 195 200 205  
 Asn Tyr Ile  
 210

&lt;210&gt; 385

&lt;211&gt; 723

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(700)

&lt;223&gt; RXN01657

&lt;400&gt; 385

cctccgtcat tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60  
 ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115  
 Val Ile Val Gly Val  
 1 5  
 tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
 10 15 20  
 ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
 25 30 35  
 ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
 40 45 50  
 ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
 55 60 65  
 gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
 70 75 80 85  
 aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
 90 95 100  
 gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451  
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
 105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
 120 125 130  
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547  
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
 135 140 145  
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
 150 155 160 165  
 caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643  
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp  
 170 175 180  
 tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691  
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu  
 185 190 195  
 ctg gcg att tgatgttttc ggtagcgctc tgt 723  
 Leu Ala Ile  
 200

&lt;210&gt; 386

&lt;211&gt; 200

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 386

Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
 1 5 10 15  
 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30  
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45  
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60  
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80  
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95  
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110  
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125  
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140  
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160

Val	Val	Gly	Val	Arg	Gln	Gly	Asn	Ile	Ile	Ala	Leu	Ser	Phe	His	Pro
				165					170					175	
Glu	Glu	Thr	Gly	Asp	Tyr	Arg	Ile	His	Gln	Ala	Trp	Leu	Asp	Leu	Val
			180					185					190		
Arg	Lys	His	Ala	Glu	Leu	Ala	Ile								
		195					200								

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<210> 387
<211> 601
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(601)  
<223> FRXA01657
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<400> 387  
cctccgtcat tgccgacgta tcccgccgcc tgggtgaagc catgggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115  
Val Ile Val Gly Val  
1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163  
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala  
10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211  
Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly  
25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259  
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys  
40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307  
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg  
55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355  
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala  
70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403  
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val  
90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451  
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe  
105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499  
Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val  
120 125 130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr  
 135 140 145  
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595  
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg  
 150 155 160 165  
 caa ggc 601  
 Gln Gly

<210> 388  
 <211> 167  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 388  
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu  
 1 5 10 15  
 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro  
 20 25 30  
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser  
 35 40 45  
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu  
 50 55 60  
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly  
 65 70 75 80  
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln  
 85 90 95  
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala  
 100 105 110  
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala  
 115 120 125  
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr  
 130 135 140  
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu  
 145 150 155 160  
 Val Val Gly Val Arg Gln Gly  
 165

<210> 389  
 <211> 897  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(874)  
 <223> RXA01098

&lt;400&gt; 389

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aaaagggctc acgatgtgct gttaagtaag attgaaaaag ttcggttgat gcatgcagat 60
gcaggtaatg accagtcggt aaatgaggag tacaagtaaa atg ggc gtg gca att 115
                                         Met Gly Val Ala Ile
                                         1 5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
                        10 15 20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala
                        25 30 35

aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc 259
Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val
                        40 45 50

acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc 307
Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg
                        55 60 65

acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc 355
Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg
                        70 75 80 85

agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt 403
Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val
                        90 95 100

tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg 451
Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu
                        105 110 115

tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg 499
Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg
                        120 125 130

cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc 547
Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr
                        135 140 145

acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca 595
Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala
                        150 155 160 165

aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg 643
Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met
                        170 175 180

gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa 691
Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys
                        185 190 195

gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc 739
Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly
                        200 205 210

aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg 787

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Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val  
 215 220 225  
 ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835  
 Leu Ala Ala Thr Ile Phe His Ph Arg Glu Val Thr Ile Ala Glu Val  
 230 235 240 245  
 aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa 884  
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys  
 250 255  
 tccacaagag tat 897

&lt;210&gt; 390

&lt;211&gt; 258

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 390

Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly  
 1 5 10 15  
 Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp  
 20 25 30  
 Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu  
 35 40 45  
 Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu  
 50 55 60  
 Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val  
 65 70 75 80  
 Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala  
 85 90 95  
 Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu  
 100 105 110  
 Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu  
 115 120 125  
 Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser  
 130 135 140  
 Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp  
 145 150 155 160  
 Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile  
 165 170 175  
 Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu  
 180 185 190  
 Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala  
 195 200 205  
 Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala  
 210 215 220



Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val  
225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val  
245 250 255

Arg Lys

<210> 391

<211> 729

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(706)

<223> RXN01104

<400> 391

cacttgcgca ctaccattgg tgtgcctgag gaaaatgatg cgtttttgga cgcagctgca 60

gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115  
Met Thr Val Ala Pro  
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451  
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
120 125 130

ggg gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
 135 140 145  
 gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
 150 155 160 165  
 gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
 170 175 180  
 ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
 185 190 195  
 act aag gga gcg ctc tagacatgaa ctcttctccc atc 729  
 Thr Lys Gly Ala Leu  
 200

&lt;210&gt; 392

&lt;211&gt; 202

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 392

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
 1 5 10 15  
 Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
 20 25 30  
 Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
 35 40 45  
 Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
 50 55 60  
 Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
 65 70 75 80  
 Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
 85 90 95  
 Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
 100 105 110  
 Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
 115 120 125  
 Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
 130 135 140  
 Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
 145 150 155 160  
 Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
 165 170 175  
 Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
195 200

<210> 393

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA01104

<400> 393

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gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115  
Met Thr Val Ala Pro  
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163  
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val  
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211  
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu  
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259  
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe  
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307  
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His  
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355  
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala  
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403  
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro  
90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451  
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro  
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499  
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile  
120 125 130

ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547  
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu  
135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595  
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg  
150 155 160 165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643  
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala  
                   170                  175                  180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691  
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser  
                   185                  190                  195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729  
 Thr Lys Gly Ala Leu  
                   200

<210> 394

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu  
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Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp  
                   20                  25                  30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly  
                   35                  40                  45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu  
           50                  55                  60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln  
           65                  70                  75                  80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala  
                   85                  90                  95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp  
                   100                  105                  110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met  
           115                  120                  125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His  
           130                  135                  140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile  
           145                  150                  155                  160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys  
                   165                  170                  175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln  
                   180                  185                  190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu  
           195                  200

<210> 395

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<211> 987
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(964)  
<223> RXN00446
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<400> 395																
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ggtgacggag gctacttggg gggctaatacg gtacccggat atg ggt gcg gtt gag																115
Met Gly Ala Val Glu																5
1																
ctc cgt gag gct ctt gca gag cat tta gag gtt gag ttt gac cag gtc																163
Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val Glu Phe Asp Gln Val																20
10 15																
acg gta ggt tgc ggc tcg tct gcg ctg tgt caa cag ctg gtt cag gca																211
Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln Gln Leu Val Gln Ala																35
25 30																
acg tgc gct cag ggc gat gag gtc att ttt cca tgg cgc agc ttt gag																259
Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro Trp Arg Ser Phe Glu																50
40 45																
gct tat cca att ttc gcg cag gtc gcg ggc gcc act cct gtt gcc att																307
Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala Thr Pro Val Ala Ile																65
55 60																
ccg ctg act gct gat cag aat cat gat ctt gat gcg atg gca gcc gcg																355
Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp Ala Met Ala Ala Ala																85
70 75 80																
atc act gat aag acc cgc ctc att ttc atc tgc aac ccc aac aat cct																403
Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys Asn Pro Asn Asn Pro																100
90 95																
tcg ggc acc acc atc acc cag gcg cag ttt gat aat ttc atg gaa aag																451
Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp Asn Phe Met Glu Lys																115
105 110																
gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat ttt gag ttc																499
Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr Phe Glu Phe																130
120 125																
aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc cac cgc cac																547
Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile His Arg His																145
135 140																
gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat ggc ctg gcg																595
Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr Gly Leu Ala																165
150 155 160																
ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc atc gca gcg																643
Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile Ile Ala Ala																180
170 175																
atg aat aag gtg gct att cct ttc gcg gtg aat tca gca gct cag gcg																691

Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala  
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739  
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val  
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787  
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala  
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835  
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala  
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883  
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe  
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931  
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys  
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtcctttgg cgttttgcgg 984  
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 280 285

tgc 987

&lt;210&gt; 396

&lt;211&gt; 288

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 396

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val  
 1 5 10 15

Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln  
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro  
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala  
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp  
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys  
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp  
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu  
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

130	135	140
Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys 145 150 155 160		
Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala 165 170 175		
Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn 180 185 190		
Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu 195 200 205		
Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val 210 215 220		
Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro 225 230 235 240		
Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile 245 250 255		
Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala 260 265 270		
Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly 275 280 285		

&lt;210&gt; 397

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(522)

&lt;223&gt; FRXA00446

&lt;400&gt; 397

atg gaa aag gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat	48
Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr	
1 5 10 15	

ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc	96
Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile	
20 25 30	

cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat	144
His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr	
35 40 45	

ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc	192
Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile	
50 55 60	

atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca	240
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Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
65 70 75 80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288  
Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn S r Ala Asp Glu Leu Met  
85 90 95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336  
Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
100 105 110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384  
Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
165 170

tagtctttgg cgttttgcgg tgc 545

&lt;210&gt; 398

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 398

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
1 5 10 15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile



130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
165 170

<210> 399  
<211> 1221  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(1198)  
<223> RXA01105

<400> 399  
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gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115  
Met Thr Lys Ile Thr  
1 5  
ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163  
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr  
10 15 20  
ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211  
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn  
25 30 35  
cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259  
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val  
40 45 50  
gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307  
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val  
55 60 65  
gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355  
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val  
70 75 80 85  
gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403  
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile  
90 95 100  
ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451  
Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu  
105 110 115  
gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499  
Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr  
120 125 130  
cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547  
His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp  
135 140 145

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt	595
Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val	
150 155 160 165	
ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac	643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp	
170 175 180	
gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat	691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp	
185 190 195	
gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg	739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu	
200 205 210	
gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct	787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala	
215 220 225	
ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg	835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala	
230 235 240 245	
ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg	883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala	
250 255 260	
ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg	931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr	
265 270 275	
ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca	979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala	
280 285 290	
cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt	
1027	
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe	
295 300 305	
gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt	
1075	
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe	
310 315 320 325	
ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg	
1123	
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu	
330 335 340	
cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca	
1171	
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala	
345 350 355	
gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca	
1218	
Ala Ala Glu Ile Ile Lys Leu Asn Leu	
360 365	

tga  
1221

<210> 400

<211> 366

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 400

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg  
1 5 10 15

Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu  
20 25 30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp  
35 40 45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro  
50 55 60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr  
65 70 75 80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn  
85 90 95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro  
100 105 110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile  
115 120 125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala  
130 135 140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys  
145 150 155 160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp  
165 170 175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly  
180 185 190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser  
195 200 205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg  
210 215 220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe  
225 230 235 240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro  
245 250 255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg  
260 265 270

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg  
 275 280 285

Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro  
 290 295 300

Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala  
 305 310 315 320

Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly  
 325 330 335

Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp  
 340 345 350

Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu  
 355 360 365

&lt;210&gt; 401

&lt;211&gt; 1449

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1426)

&lt;223&gt; RXA01106

&lt;400&gt; 401

ggtaaacaatg cgggcttaag aacttggtgtt gagggccgctt ggattcgggc accgagctcg 60

aagaatttcg attcaacctt ttaagggaga acttttcgcc atg ttg aat gtc act 115  
 Met Leu Asn Val Thr  
 1 5

gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163  
 Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu  
 10 15 20

cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211  
 Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro  
 25 30 35

gtt gta gaa gat gtc caa aac cgc ggc gct gaa gct gct ttg gat tac 259  
 Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr  
 40 45 50

ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307  
 Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala  
 55 60 65

gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355  
 Glu Val Ile Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu  
 70 75 80 85

tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403  
 Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln  
 90 95 100

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act	451
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr	
105 110 115	
gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc	499
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly	
120 125 130	
aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa	547
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln	
135 140 145	
gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag	595
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu	
150 155 160 165	
cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg	643
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu	
170 175 180	
ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	
1027	
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	
1075	
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	
1123	
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	

330 335 340  
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc  
 1171  
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly  
 345 350 355  
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac  
 1219  
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His  
 360 365 370  
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg  
 1267  
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr  
 375 380 385  
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct  
 1315  
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala  
 390 395 400 405  
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat  
 1363  
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp  
 410 415 420  
 ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc  
 1411  
 Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro  
 425 430 435  
 acc acc gac gag gcc taagaaaaat gaccaaaatt act  
 1449  
 Thr Thr Asp Glu Ala  
 440

<210> 402  
 <211> 442  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 402  
 Met Leu Asn Val Thr Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp  
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 Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu  
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 Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu  
 35 40 45  
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser  
 50 55 60  
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp  
 65 70 75 80  
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys  
 85 90 95

Val His Ala Glu Gln Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro  
 100 105 110  
 Gly Gly Thr Val Thr Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu  
 115 120 125  
 Tyr Val Pro Gly Gly Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn  
 130 135 140  
 Thr Val Pro Ala Gln Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser  
 145 150 155 160  
 Pro Pro Gln Ala Glu His Gly Gly Trp Pro His Pro Thr Ile Leu Ala  
 165 170 175  
 Ala Cys Ser Ile Leu Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly  
 180 185 190  
 Gln Ala Val Ala Leu Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu  
 195 200 205  
 Pro Val Asp Met Ile Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala  
 210 215 220  
 Lys Arg Leu Val Arg Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro  
 225 230 235 240  
 Thr Glu Ile Ala Val Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val  
 245 250 255  
 Ala Tyr Asp Leu Ile Ser Gln Ala Glu His Asp Val Met Ala Ala Ser  
 260 265 270  
 Val Leu Ile Thr Asp Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu  
 275 280 285  
 Ile Glu Ala Arg Tyr Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu  
 290 295 300  
 Ala Leu Arg Gly Ala Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser  
 305 310 315 320  
 Val Gly Ile Gln Val Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile  
 325 330 335  
 His Thr Glu Asn Ala Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly  
 340 345 350  
 Ala Ile Phe Val Gly Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser  
 355 360 365  
 Ala Gly Ser Asn His Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser  
 370 375 380  
 Ala Gly Leu Ser Thr His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu  
 385 390 395 400  
 Tyr Asp Glu Ala Ala Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe  
 405 410 415

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg  
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala  
 435 440

<210> 403

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXC00930

<400> 403

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ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115  
 Met Ser Gly His Ser  
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163  
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg  
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211  
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg  
 25 30 35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259  
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile  
 40 45 50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307  
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala  
 55 60 65

cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355  
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn  
 70 75 80 85

atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403  
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu  
 90 95 100

tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451  
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala  
 105 110 115

atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499  
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr  
 120 125 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547  
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser  
 135 140 145

gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595



Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val  
 150 155 160 165  
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643  
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile  
 170 175 180  
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691  
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp  
 185 190 195  
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739  
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp  
 200 205 210  
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787  
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp  
 215 220 225  
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835  
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu  
 230 235 240 245  
 aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876  
 Thr Glu Leu Glu Asn Asp  
 250

&lt;210&gt; 404

&lt;211&gt; 251

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 404

Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala  
 1 5 10 15  
 Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile  
 20 25 30  
 Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr  
 35 40 45  
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp  
 50 55 60  
 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly  
 65 70 75 80  
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val  
 85 90 95  
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr  
 100 105 110  
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser  
 115 120 125  
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln  
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala  
 145 150 155 160  
 Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys  
 165 170 175  
 Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly  
 180 185 190  
 Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val  
 195 200 205  
 Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala  
 210 215 220  
 Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu  
 225 230 235 240  
 Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp  
 245 250

&lt;210&gt; 405

&lt;211&gt; 547

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(547)

&lt;223&gt; RXC01096

&lt;400&gt; 405

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gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115  
 Met Lys Pro Arg Val  
 1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163  
 Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser  
 10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211  
 Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly  
 25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259  
 Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met  
 40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307  
 Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu  
 55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355  
 Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala  
 70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403  
 Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

90	95	100	
gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag			451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys			
105	110	115	
gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc			499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr			
120	125	130	
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta			547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu			
135	140	145	

&lt;210&gt; 406

&lt;211&gt; 149

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 406

Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu			
1	5	10	15
Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe			
20	25	30	
Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp			
35	40	45	
Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala			
50	55	60	
Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile			
65	70	75	80
Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu			
85	90	95	
Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly			
100	105	110	
Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala			
115	120	125	
Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met			
130	135	140	
Ile Gly Cys Ala Leu			
145			

&lt;210&gt; 407

&lt;211&gt; 1020

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(997)

&lt;223&gt; RXC01656



Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val  
 215 220 225

cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835  
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys  
 230 235 240 245

tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883  
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr  
 250 255 260

ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931  
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly  
 265 270 275

gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979  
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg  
 280 285 290

ctc gcc gag cgc ggc tgg tgatcgttg agtttttagct ctc  
 1020  
 Leu Ala Glu Arg Gly Trp  
 295

&lt;210&gt; 408

&lt;211&gt; 299

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 408

Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg  
 1 5 10 15

Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr  
 20 25 30

Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met  
 35 40 45

Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala  
 50 55 60

Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser  
 65 70 75 80

Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln  
 85 90 95

Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu  
 100 105 110

Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val  
 115 120 125

Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile  
 130 135 140

Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly  
 145 150 155 160

Asp	Val	Ser	Glu	Ala	Val	Arg	His	Leu	Arg	Thr	Ile	Arg	Gly	Asp	Ile	
			165						170			175				
Asn	Arg	Leu	Arg	Ser	Leu	Asp	Glu	Asp	Glu	Leu	Phe	Val	Ala	Ala	Lys	
			180						185			190				
Glu	Phe	Gln	Ala	Pro	Tyr	Asp	Leu	Val	Arg	Glu	Val	Ala	Ser	Thr	Gly	
			195						200			205				
Lys	Leu	Pro	Val	Val	Thr	Phe	Val	Ala	Gly	Gly	Val	Ala	Thr	Pro	Ala	
			210						215			220				
Asp	Ala	Ala	Leu	Val	Arg	Gln	Met	Gly	Ala	Glu	Gly	Val	Phe	Val	Gly	
225						230						235			240	
Ser	Gly	Ile	Phe	Lys	Ser	Gly	Asn	Pro	Ala	Ala	Arg	Ala	Ala	Ala	Ile	
			245						250			255				
Val	Lys	Ala	Ala	Thr	Leu	Phe	Asp	Asp	Pro	Ser	Val	Ile	Ala	Asp	Val	
			260						265			270				
Ser	Arg	Gly	Leu	Gly	Glu	Ala	Met	Val	Gly	Ile	Asn	Val	Ser	Asp	Val	
			275						280			285				
Pro	Ala	Pro	His	Arg	Leu	Ala	Glu	Arg	Gly	Trp						
290						295										

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<210> 409
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1042)
<223> RXC01158
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agttatctca aaaaagaaga agaagtctcc tacgggagag																	
											atg	tcc	att	ggt	gag		115
											Met	Ser	Ile	Val	Glu		
											1				5		
cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc																	163
His	Ile	Lys	Glu	Phe	Arg	Arg	Arg	Leu	Leu	Ile	Ala	Leu	Ala	Gly	Ile		
				10					15					20			
ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg																	211
Leu	Val	Gly	Thr	Ile	Ile	Gly	Phe	Ile	Trp	Tyr	Asp	Phe	Ser	Phe	Trp		
			25					30					35				
cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg																	259
Gln	Ile	Pro	Thr	Leu	Gly	Glu	Leu	Leu	Arg	Asp	Pro	Tyr	Cys	Ser	Leu		
		40					45					50					
cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg																	307
Pro	Ala	Glu	Ser	Arg	Trp		Met	Ser	Asp	Ser	Glu	Glu	Cys	Arg	Leu		
	55					60					65						

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg	355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala	
70 75 80 85	
gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu	
90 95 100	
tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105 110 115	
gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val	
120 125 130	
ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135 140 145	
ggg gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga	595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150 155 160 165	
ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca	643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro	
170 175 180	
ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185 190 195	
att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala	
200 205 210	
gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala	
215 220 225	
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230 235 240 245	
aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250 255 260	
gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265 270 275	
cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu	
280 285 290	
aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp	
295 300 305	

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta  
 1065  
 Phe Gly Asp Val Leu  
 310

<210> 410  
 <211> 314  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 410  
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                   20                  25                  30  
 Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp  
           35                  40                  45  
 Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser  
       50                  55                  60  
 Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu  
   65                  70                  75                  80  
 Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val  
                   85                  90                  95  
 Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn  
           100                  105                  110  
 Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe  
       115                  120                  125  
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu  
   130                  135                  140  
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly  
  145                  150                  155                  160  
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val  
           165                  170                  175  
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile  
       180                  185                  190  
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile  
       195                  200                  205  
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr  
   210                  215                  220  
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu  
  225                  230                  235                  240  
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu  
           245                  250                  255  
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala



260	265	270	
Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu			
275	280	285	
Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys			
290	295	300	
Pro Gly Arg Ala Asp Phe Gly Asp Val Leu			
305	310		
<210> 411			
<211> 1413			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1390)			
<223> RXA02458			
<400> 411			
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ggtggtgaac aaaacaaatc ttccacacat aacatctatt atg gtc ttt gtg tct	115		
	Met Val Phe Val Ser		
	1	5	
gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc	163		
Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly			
10	15	20	
ccc ata gtc tcg gac ctg gct atc cct ggt tcc aag tcg atc acc aac	211		
Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn			
25	30	35	
cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att	259		
Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile			
40	45	50	
gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc	307		
Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg			
55	60	65	
agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt	355		
Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val			
70	75	80	85
gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt	403		
Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly			
90	95	100	
acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct	451		
Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro			
105	110	115	
gtt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc	499		
Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser			
120	125	130	

att ttg gat gcg ctg cgt tcg ctt ggt gtg gag gta gac aac aac aat	547
Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn	
135 140 145	
ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt	595
Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val	
150 155 160 165	
gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt	643
Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu	
170 175 180	
tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt	691
Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly	
185 190 195	
cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt	739
Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg	
200 205 210	
tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat	787
Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His	
215 220 225	
cct ggt gag atc ttg ggt cgg acc tgg cgc att gag ccg gat ctt tct	835
Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser	
230 235 240 245	
aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc	883
Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile	
250 255 260	
aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att	931
Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile	
265 270 275	
cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag	979
Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln	
280 285 290	
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1027	
Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly	
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1075	
Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala	
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1123	
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330 335 340	
cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag	
1171	
His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu	
345 350 355	

atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg  
1219

Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu  
360 365 370

att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat  
1267

Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp  
375 380 385

cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc  
1315

His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly  
390 395 400 405

gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt  
1363

Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe  
410 415 420

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425 430

ccg  
1413

<210> 412

<211> 430

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 412

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Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr  
35 40 45

Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met  
50 55 60

Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val  
65 70 75 80

Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu  
85 90 95

Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala  
100 105 110

Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val  
115 120 125

Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu  
130 135 140

Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro  
 145 150 155 160  
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val  
 165 170 175  
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val  
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 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr  
 195 200 205  
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn  
 210 215 220  
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile  
 225 230 235 240  
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Ala Val  
 245 250 255  
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln  
 260 265 270  
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val  
 275 280 285  
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro  
 290 295 300  
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu  
 305 310 315 320  
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg  
 325 330 335  
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala  
 340 345 350  
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu  
 355 360 365  
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp  
 370 375 380  
 His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly  
 385 390 395 400  
 Leu Ala Val Asp Gly Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys  
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 Thr Phe Pro Gly Phe Glu Asn Val Trp Glu Glu Met Val Gly  
 420 425 430

&lt;210&gt; 413

&lt;211&gt; 1266

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1243)

&lt;223&gt; RXA02790

&lt;400&gt; 413

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                                         Met Glu Pro Val Tyr
                                         1           5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
                        10                        15                        20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
                        25                        30                        35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
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Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu
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Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser
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Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln
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gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp
105                        110                        115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp
120                        125                        130

gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc 547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile
135                        140                        145

gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag 595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu
150                        155                        160                        165

gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc 643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val
170                        175                        180

cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys
185                        190                        195

cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc 739

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Arg	Leu	Glu	Gly	Leu	Ile	Met	Pro	Gly	Gln	Tyr	Val	Val	Asp	Pro	Ser		
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aac	gac	gcc	cag	gga	atc	ctc	acc	gat	ctg	atc	acg	cga	tca	gca	aac	787	
Asn	Asp	Ala	Gln	Gly	Ile	Leu	Thr	Asp	Leu	Ile	Thr	Arg	Ser	Ala	Asn		
	215					220					225						
cat	ttc	caa	gaa	acc	gac	atc	acg	ggc	cgt	gca	gat	gcc	atc	gga	ctt	835	
His	Phe	Gln	Glu	Thr	Asp	Ile	Thr	Gly	Arg	Ala	Asp	Ala	Ile	Gly	Leu		
	230				235				240					245			
act	cca	tat	gag	ctg	gtc	acc	gca	gca	tct	tta	atc	gag	cgc	gaa	gca	883	
Thr	Pro	Tyr	Glu	Leu	Val	Thr	Ala	Ala	Ser	Leu	Ile	Glu	Arg	Glu	Ala		
				250					255					260			
cca	gca	gga	gat	ttt	gat	aag	gtc	gcc	cgc	gtc	atc	ttg	aac	cgt	ctc	931	
Pro	Ala	Gly	Asp	Phe	Asp	Lys	Val	Ala	Arg	Val	Ile	Leu	Asn	Arg	Leu		
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gcc	gag	cca	atg	cag	ctg	caa	ttc	gac	tcc	acc	gtc	aac	tac	ggg	ctg	979	
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cca	tgg	aac	act	tac	gcc	atg	gac	ggc	ctg	cca	caa	acc	ccc	atc	gcc		
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Pro	Trp	Asn	Thr	Tyr	Ala	Met	Asp	Gly	Leu	Pro	Gln	Thr	Pro	Ile	Ala		
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1123																	
Ala	Val	Ser	Thr	Glu	Ala	Leu	Gln	Ala	Met	Glu	Asn	Pro	Ala	Glu	Gly		
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1171																	
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			345					350					355				
aac	gac	acc	ttc	gaa	gag	cac	gaa	gcc	gac	att	gag	caa	gct	ttg	aac		
1219																	
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		360					365					370					
agt	ggc	gtt	cta	gac	agc	aac	cga	taaggatcag	cgaataaaaat	tgg							
1266																	
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<213>	Corynebacterium glutamicum																
<400>	414																
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Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly	35	40	45
Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu	50	55	60
Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe	65	70	75
Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly	85	90	95
Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala	100	105	110
Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly	115	120	125
Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly	130	135	140
Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn	145	150	155
Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro	165	170	175
Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg	180	185	190
Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr	195	200	205
Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile	210	215	220
Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala	225	230	235
Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu	245	250	255
Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val	260	265	270
Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr	275	280	285
Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp	290	295	300
Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro	305	310	315
Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu	325	330	335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp  
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile  
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Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg  
 370 375 380

&lt;210&gt; 415

&lt;211&gt; 644

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(621)

&lt;223&gt; RXN00954

&lt;400&gt; 415

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1				5				10						15		
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Ala	Tyr	Asn	Pro	Ala	Ile	Ala	His	Val	Gln	Pro	Val	Arg	Gln	Ala	Leu	
			20					25					30			
aaa	ttc	ccc	acc	atc	ttc	aac	acg	ctt	gga	cca	ttg	ctg	tcc	ccg	gcg	144
Lys	Phe	Pro	Thr	Ile	Phe	Asn	Thr	Leu	Gly	Pro	Leu	Leu	Ser	Pro	Ala	
		35					40					45				
cgc	ccg	gag	cgt	cag	atc	atg	ggc	gtg	gcc	aat	gcc	aat	cat	gga	cag	192
Arg	Pro	Glu	Arg	Gln	Ile	Met	Gly	Val	Ala	Asn	Ala	Asn	His	Gly	Gln	
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ctc	atc	gcc	gag	gtc	ttc	cgc	gag	ttg	ggc	cgt	aca	cgc	gcg	ctt	gtt	240
Leu	Ile	Ala	Glu	Val	Phe	Arg	Glu	Leu	Gly	Arg	Thr	Arg	Ala	Leu	Val	
65				70				75						80		
gtg	cat	ggc	gca	ggc	acc	gat	gag	atc	gca	gtc	cac	ggc	acc	acc	ttg	288
Val	His	Gly	Ala	Gly	Thr	Asp	Glu	Ile	Ala	Val	His	Gly	Thr	Thr	Leu	
				85				90					95			
gtg	tgg	gag	ctt	aaa	gaa	gac	ggc	acc	atc	gag	cat	tac	acc	atc	gag	336
Val	Trp	Glu	Leu	Lys	Glu	Asp	Gly	Thr	Ile	Glu	His	Tyr	Thr	Ile	Glu	
		100					105					110				
cct	gag	gac	ctt	ggc	ctt	ggc	cgc	tac	acc	ctt	gag	gat	ctc	gta	ggt	384
Pro	Glu	Asp	Leu	Gly	Leu	Gly	Arg	Tyr	Thr	Leu	Glu	Asp	Leu	Val	Gly	
		115					120					125				
ggc	ctc	ggc	act	gag	aac	gcc	gaa	gct	atg	cgc	gct	act	ttc	gcg	ggc	432
Gly	Leu	Gly	Thr	Glu	Asn	Ala	Glu	Ala	Met	Arg	Ala	Thr	Phe	Ala	Gly	
	130					135					140					
acc	ggc	cct	gat	gca	cac	cgt	gat	gcg	ttg	gct	gcg	tcc	gca	ggt	gcg	480
Thr	Gly	Pro	Asp	Ala	His	Arg	Asp	Ala	Leu	Ala	Ala	Ser	Ala	Gly	Ala	
145					150			155						160		



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 180 185 190  
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 Lys His Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp  
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 <211> 207  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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 Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala  
 35 40 45  
 Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln  
 50 55 60  
 Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val  
 65 70 75 80  
 Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu  
 85 90 95  
 Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu  
 100 105 110  
 Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly  
 115 120 125  
 Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly  
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 Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala  
 145 150 155 160  
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln  
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<210> 417  
 <211> 611  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(588)  
 <223> FRXA00954

<400> 417  
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 gtt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca 96  
 Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro  
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 Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
 35 40 45  
 gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt 192  
 Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
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 Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
 65 70 75 80  
 cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag 288  
 His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
 85 90 95  
 cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt 336  
 His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
 100 105 110  
 gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc 384  
 Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
 115 120 125  
 gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct 432  
 Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
 130 135 140  
 gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg 480  
 Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
 145 150 155 160  
 aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc 528  
 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
 165 170 175  
 cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag 576  
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 tct tcc aat gac tagtaataat ctgccacag tgt 611

Ser Ser Asn Asp  
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<210> 418  
<211> 196  
<212> PRT  
<213> Corynebacterium glutamicum

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Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro  
20 25 30  
Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn  
35 40 45  
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg  
50 55 60  
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val  
65 70 75 80  
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu  
85 90 95  
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu  
100 105 110  
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg  
115 120 125  
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala  
130 135 140  
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu  
145 150 155 160  
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr  
165 170 175  
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu  
180 185 190  
Ser Ser Asn Asp  
195

<210> 419  
<211> 1677  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101) .. (1654)  
<223> RXN00957

<400> 419

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aaggcttcag ccccaaatg atttcctcgg taggtgcccc atg agc acg aat ccc 115  
Met Ser Thr Asn Pro  
1 5  
cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163  
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu  
10 15 20  
ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211  
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu  
25 30 35  
agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259  
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu  
40 45 50  
aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307  
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln  
55 60 65  
ccg ctg acg gac tcg ggt agg gca gtg gtt gcg cgc cta acg cag cag 355  
Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln  
70 75 80 85  
ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403  
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser  
90 95 100  
gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451  
Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu  
105 110 115  
gtg ctg cgc aag ttg cag ttc gag tcc ggt tac agc gac gcg tcc ctg 499  
Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu  
120 125 130  
cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547  
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu  
135 140 145  
acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595  
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln  
150 155 160 165  
ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643  
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr  
170 175 180  
gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag 691  
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu  
185 190 195  
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa 739  
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu  
200 205 210  
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg 787  
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val  
215 220 225

gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa 835  
 Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys  
 230 235 240 245

gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act 883  
 Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr  
 250 255 260

ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt 931  
 Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg  
 265 270 275

gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa 979  
 Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu  
 280 285 290

ggc cgc tcc tat gaa ctt ttt ggc gca tcc cct gag tcc aac ctc aag  
 1027  
 Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro Glu Ser Asn Leu Lys  
 295 300 305

ttc acc gct gct aac cgt gag ctg cag ctg tac cca atc gca ggt acc  
 1075  
 Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr Pro Ile Ala Gly Thr  
 310 315 320 325

cgc ccc cgt gga ctc aac cca gat ggc tcc atc aac gat gag cta gat  
 1123  
 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp  
 330 335 340

atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag  
 1171  
 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu  
 345 350 355

cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg  
 1219  
 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser  
 360 365 370

gtc cca gcg tcg cgc cgg gtt gcg gat ctt ttg cag gtg gat cgc tat  
 1267  
 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr  
 375 380 385

tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca  
 1315  
 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro  
 390 395 400 405

gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg  
 1363  
 Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr  
 410 415 420

ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc  
 1411  
 Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val  
 425 430 435

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc  
1459

Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg  
440 445 450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc  
1507

Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val  
455 460 465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat  
1555

Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp  
470 475 480 485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc  
1603

Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala  
490 495 500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc  
1651

Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile  
505 510 515

cga tgacacacgt tgttctcatt gat  
1677

Arg

<210> 420

<211> 518

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met Ser Thr Asn Pro His Val Phe Ser Leu Asp Val Arg Tyr His Glu  
1 5 10 15

Asp Ala Ser Ala Leu Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp  
20 25 30

Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser  
35 40 45

Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn  
50 55 60

Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala  
65 70 75 80

Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe  
85 90 95

Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala  
100 105 110

Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr  
115 120 125

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe  
 130 135 140  
 Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr  
 145 150 155 160  
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn  
 165 170 175  
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly  
 180 185 190  
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala  
 195 200 205  
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp  
 210 215 220  
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln  
 225 230 235 240  
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val  
 245 250 255  
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala  
 260 265 270  
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile  
 275 280 285  
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro  
 290 295 300  
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr  
 305 310 315 320  
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile  
 325 330 335  
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala  
 340 345 350  
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp  
 355 360 365  
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu  
 370 375 380  
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr  
 385 390 395 400  
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys  
 405 410 415  
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu  
 420 425 430  
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala  
 435 440 445

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile  
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala  
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu  
 485 490 495

His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser  
 500 505 510

Thr Leu Glu Val Ile Arg  
 515

&lt;210&gt; 421

&lt;211&gt; 1151

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1128)

&lt;223&gt; FRXA00957

&lt;400&gt; 421

gat ttc tta gaa acc ttt gaa acg ctc ccc gct gtc gag gag agc gtc	48
Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val	
1 5 10 15	
aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac	96
Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp	
20 25 30	
atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc	144
Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala	
35 40 45	
cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac	192
Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp	
50 55 60	
gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac	240
Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp	
65 70 75 80	
ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc	288
Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg	
85 90 95	
acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac	336
Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr	
100 105 110	
caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc	384
Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe	
115 120 125	
gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc	432
Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe	



130	135	140	
tat atc cgt ggc ctc aac gaa ggc cgc tcc tat gaa ctt ttt ggc gca			480
Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala			
145	150	155	160
tcc cct gag tcc aac ctc aag ttc acc gct gct aac cgt gag ctg cag			528
Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln			
	165	170	175
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc			576
Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly			
	180	185	190
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act			624
Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr			
	195	200	205
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc			672
Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg			
	210	215	220
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat			720
Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp			
	225	230	240
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt			768
Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg			
	245	250	255
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg			816
Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg			
	260	265	270
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct			864
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala			
	275	280	285
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt			912
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly			
	290	295	300
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att			960
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile			
	305	310	315
gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct			
1008			
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala			
	325	330	335
ggt gct ggt gtg gtc cgc gat tct aat cct caa tct gaa gcc gat gag			
1056			
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu			
	340	345	350
acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct			
1104			
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala			
	355	360	365

ggt tcc act ttg gag gtc atc cga tgacacacgt tgttttcatt gat  
1151

Gly Ser Thr Leu Glu Val Ile Arg  
370 375

<210> 422

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val  
1 5 10 15

Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp  
20 25 30

Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala  
35 40 45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp  
50 55 60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp  
65 70 75 80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg  
85 90 95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr  
100 105 110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe  
115 120 125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe  
130 135 140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala  
145 150 155 160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln  
165 170 175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly  
180 185 190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr  
195 200 205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg  
210 215 220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp  
225 230 235 240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg  
245 250 255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg

260	265	270
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala		
275	280	285
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly		
290	295	300
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile		
305	310	315
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala		
325	330	335
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu		
340	345	350
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala		
355	360	365
Gly Ser Thr Leu Glu Val Ile Arg		
370	375	
<210> 423		
<211> 1068		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(1045)		
<223> RXA02687		
<400> 423		
caaaaccatg ctcggcgggg gagagttggg ccaagcgggt cgctaattga gcaacagaca 60		
tggacaccca ccttagttcg gcgggttaag ctgtgtaacc atg agc gac gca cca	115	
	Met Ser Asp Ala Pro	
	1 5	
act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc	163	
Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala		
10 15 20		
ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag	211	
Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu		
25 30 35		
cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac	259	
Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His		
40 45 50		
ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc	307	
Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly		
55 60 65		
ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa	355	
Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln		
70 75 80 85		

atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403  
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg  
 90 95 100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451  
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val  
 105 110 115

ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499  
 Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala  
 120 125 130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547  
 Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala  
 135 140 145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595  
 Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu  
 150 155 160 165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643  
 Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala  
 170 175 180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691  
 Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro  
 185 190 195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739  
 Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro  
 200 205 210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787  
 Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp  
 215 220 225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835  
 Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr  
 230 235 240 245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883  
 Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala  
 250 255 260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931  
 Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val  
 265 270 275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979  
 Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp  
 280 285 290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc  
 1027  
 Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser  
 295 300 305

gaa gga agg aaa ctt aac tagccatggc cggccggatt att  
 1068  
 Glu Gly Arg Lys Leu Asn  
 310 315

&lt;210&gt; 424

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 424

Met Ser Asp Ala Pro Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr  
 1 5 10 15

Phe Thr Glu Glu Ala Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly  
 20 25 30

Asp Gly Glu Ile Glu Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val  
 35 40 45

Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu  
 50 55 60

Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln  
 65 70 75 80

Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe  
 85 90 95

Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu  
 100 105 110

Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr  
 115 120 125

Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly  
 130 135 140

Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser  
 145 150 155 160

Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala  
 165 170 175

Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala  
 180 185 190

Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser  
 195 200 205

Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala  
 210 215 220

Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys  
 225 230 235 240

Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg  
 245 250 255

Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu  
 260 265 270

Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser  
 275 280 285

Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp  
 290 295 300

Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn  
 305 310 315

<210> 425

<211> 1353

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> RXN01698

<400> 425

cgctagtgcc tgcagttatg tcgctttttg acgtcgaaaa gcaatttttaa aaagcccttg 60

gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115  
 Met Leu Gly Met Leu  
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163  
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr  
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211  
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser  
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259  
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met  
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307  
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly  
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355  
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp  
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403  
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp  
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451  
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr  
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499  
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly  
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547  
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr  
 135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa 595  
 Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu  
 150 155 160 165

acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc 643  
 Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser  
 170 175 180

gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc 691  
 Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile  
 185 190 195

gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg 739  
 Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Glu Ser Met  
 200 205 210

atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc 787  
 Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly  
 215 220 225

atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac 835  
 Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His  
 230 235 240 245

att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg 883  
 Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met  
 250 255 260

ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa 931  
 Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu  
 265 270 275

gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac 979  
 Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp  
 280 285 290

aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc  
 1027  
 Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly  
 295 300 305

atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att  
 1075  
 Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile  
 310 315 320 325

tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag  
 1123  
 Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys  
 330 335 340

gca gca acc gga atc cac cag cgt tcc gac gtg tgc gct gtt cca gcc  
 1171  
 Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala  
 345 350 355

gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca  
 1219  
 Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala  
 360 365 370

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac  
1267

Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn  
375 380 385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt  
1315

Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly  
390 395 400 405

tta gag gat gga gcg taatgaagtg aatgatcaaa ttc  
1353

Leu Glu Asp Gly Ala  
410

<210> 426

<211> 410

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 426

Met Leu Gly Met Leu Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln  
1 5 10 15

Ala Leu Ile Ala Thr Val Glu His Met Pro Ala Gly Val Pro Val Thr  
20 25 30

Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly  
35 40 45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr  
50 55 60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile  
65 70 75 80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
85 90 95

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
100 105 110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
115 120 125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
130 135 140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
145 150 155 160

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
165 170 175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
180 185 190

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
195 200 205



Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 210 215 220

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 225 230 235 240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 245 250 255

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 260 265 270

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu  
 275 280 285

Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly  
 290 295 300

Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala  
 305 310 315 320

Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp  
 325 330 335

Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val  
 340 345 350

Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu  
 355 360 365

Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 370 375 380

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 385 390 395 400

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 405 410

&lt;210&gt; 427

&lt;211&gt; 1013

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(990)

&lt;223&gt; FRXA01698

&lt;400&gt; 427

ggc aac act gag tgg gat aag tgg acc acc atc atg tcc tct gac gct 48  
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
 1 5 10 15

ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg 96  
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
 20 25 30

ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144  
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly

35	40	45	
atg ctc aag tac gga ttc gat gat gcc cgc aac gtg ctg gag cgt tct Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser 50 55 60			192
tca gcc cgt gag acg gca gca cgc gtg gca gca gca acc gtt gcg cgt Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg 65 70 75 80			240
tcc ttc ctg cgt gaa acc ttg ggc gtg gaa gtg ctt tcc cac gta att Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile 85 90 95			288
tcc att ggt gcg tcc gag cct tac act ggc gcg gag cca acc ttt gca Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala 100 105 110			336
gat att caa gca atc gat gat tcc cca gtt cgt gca ttc ggt aaa gac Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp 115 120 125			384
gct gaa gaa tcc atg atc gcg gaa atc gag gcc gca aag aaa gcc ggc Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly 130 135 140			432
gat acc ctc ggt ggc atc gtg gaa gtg att gtt gaa ggc ctg ccc atc Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile 145 150 155 160			480
ggt ttg ggc tca cac att tct ggc gaa gat cgc ctc gat gcg cag atc Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile 165 170 175			528
gca gct gca ctc atg ggc att cag gcc atc aag ggc gtg gaa atc ggt Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly 180 185 190			576
gac ggt ttc gaa gaa gct cgt cga cgt ggc tcc gaa gcc cac gat gaa Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu 195 200 205			624
gtg ttc ctg gat gac aac ggc gta tac cgc aac acc aac cgt gca ggt Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220			672
ggc ctc gaa ggc ggc atg acc aac ggt gaa acc ctg cgc gtt cgt gct Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 235 240			720
ggc atg aag cca att tct act gtg cct cgc gcc ctg aaa acc att gat Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255			768
atg gaa aac ggc aag gca gca acc gga atc cac cag cgt tcc gac gtg Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270			816
tgc gct gtt cca gcc gcc ggt gtc gtt gca gaa gca atg gtc acc ctg Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285			864

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912  
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser  
 290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960  
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg  
 305 310 315 320

atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa  
 1010  
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala  
 325 330

ttc  
 1013

<210> 428

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 428

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala  
 1 5 10 15

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg  
 20 25 30

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly  
 35 40 45

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser  
 50 55 60

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg  
 65 70 75 80

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile  
 85 90 95

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala  
 100 105 110

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp  
 115 120 125

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly  
 130 135 140

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile  
 145 150 155 160

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile  
 165 170 175

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly  
 180 185 190

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu

195	200	205
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220		
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 235 240		
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255		
Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270		
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285		
Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser 290 295 300		
Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg 305 310 315 320		
Met Lys Phe Glu Gly Leu Glu Asp Gly Ala 325 330		

&lt;210&gt; 429

&lt;211&gt; 906

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(883)

&lt;223&gt; RXA01095

&lt;400&gt; 429

gaaaccccag gtcaaagcta ggggtgtggca ccctgatttc tttcgccatg tgtgttcggg 60

ataaccttaa acacagcatt gggttgaagg aggttggggc atg gtt gca aca gag	115
Met Val Ala Thr Glu	
1 5	

aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca	163
Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala	
10 15 20	

acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc	211
Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu	
25 30 35	

acg gcg gct ttc gat att gct tca gtc ttt ttt tcg tct gga tgt aat	259
Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn	
40 45 50	

gtc gta gtc gcc ttt gat cgt ttt gca tcc aat tgg tct gat cat tcg	307
Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser	
55 60 65	

gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg	355
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Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met
 70              75              80              85

ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat    403
Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp
              90              95              100

atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat    451
Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp
              105              110              115

ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc    499
Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile
              120              125              130

gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa    547
Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu
              135              140              145

tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct    595
Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser
              150              155              160              165

gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca    643
Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr
              170              175              180

gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct    691
Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro
              185              190              195

gaa gcg ttt tcg ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc    739
Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg
              200              205              210

att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca    787
Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala
              215              220              225

cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc    835
Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr
              230              235              240              245

aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tcg cgt    883
Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg
              250              255              260

tgaagagggtg ctctgtgggtc agc    906

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&lt;210&gt; 430

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 430

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Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile
  1              5              10              15

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Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser
      20              25              30

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Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe  
                   35                                  40                                  45  
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn  
                   50                                  55                                  60  
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly  
                   65                                  70                                  75                                  80  
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp  
                                   85                                  90                                  95  
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro  
                                   100                                  105                                  110  
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala  
                   115                                  120                                  125  
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu  
                   130                                  135                                  140  
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met  
                   145                                  150                                  155                                  160  
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val  
                                   165                                  170                                  175  
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly  
                                   180                                  185                                  190  
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro  
                   195                                  200                                  205  
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu  
                   210                                  215                                  220  
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His  
                   225                                  230                                  235                                  240  
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro  
                                   245                                  250                                  255  
 Ala Cys Pro Ser Arg  
                                   260

&lt;210&gt; 431

&lt;211&gt; 1545

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1522)

&lt;223&gt; RXA00955

&lt;400&gt; 431

gatggtgcac aaaaggcgct ttccttgctt gccgacggca ccacccaggc atggttggcc 60

aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115

																	Met Thr Ser Asn Asn 1 5
ctg ccc aca gtg ttg gaa agc atc gtc gag ggt cgt cgc gga cac ctg	163																
Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly Arg Arg Gly His Leu																	
10 15 20																	
gag gaa att cgc gct cgc atc gct cac gtg gat gtg gat gcg ctt cca	211																
Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp Val Asp Ala Leu Pro																	
25 30 35																	
aaa tcc acc cgt tct ctg ttt gat tcc ctc aac cag ggt agg gga ggg	259																
Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn Gln Gly Arg Gly Gly																	
40 45 50																	
gcg cgt ttc atc atg gag tgc aag tcc gca tcg cct tct ttg gga atg	307																
Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser Pro Ser Leu Gly Met																	
55 60 65																	
att cgt gag cac tac cag ccg ggt gaa atc gct cgc gtg tac tct cgc	355																
Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala Arg Val Tyr Ser Arg																	
70 75 80 85																	
tac gcc agc ggc att tcc gtg ctg tgc gag ccg gat cgt ttt ggt ggc	403																
Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro Asp Arg Phe Gly Gly																	
90 95 100																	
gat tac gat cac ctc gct acc gtt gcc gct acc tct cat ctt ccg gtg	451																
Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr Ser His Leu Pro Val																	
105 110 115																	
ctg tgc aaa gac ttc atc att gat cct gtc cag gta cac gcg gcg cgt	499																
Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln Val His Ala Ala Arg																	
120 125 130																	
tac ttt ggt gct gat gcc atc ctg ctc atg ctc tct gtg ctt gat gat	547																
Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu Ser Val Leu Asp Asp																	
135 140 145																	
gaa gag tac gca gca ctc gct gcc gag gct gcg cgt ttt gat ctg gat	595																
Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala Arg Phe Asp Leu Asp																	
150 155 160 165																	
atc ctc acc gag gtt att gat gag gag gaa gtc gcc cgc gcc atc aag	643																
Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val Ala Arg Ala Ile Lys																	
170 175 180																	
ctg ggt gcg aag atc ttt ggc gtc aac cac cgc aac ctg cat gat ctg	691																
Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg Asn Leu His Asp Leu																	
185 190 195																	
tcc att gat ttg gat cgt tca cgt cgc ctg tcc aag ctc att cca gca	739																
Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser Lys Leu Ile Pro Ala																	
200 205 210																	
gat gcc gtg ctc gtg tct gag tct ggc gtg cgc gat acc gaa acc gtc	787																
Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg Asp Thr Glu Thr Val																	
215 220 225																	
cgc cag cta ggt ggg cac tcc aat gca ttc ctc gtt ggc tcc cag ctg	835																
Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu Val Gly Ser Gln Leu																	

230	235	240	245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc				883
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly				
250		255	260	
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct				931
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala				
265		270	275	
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg				979
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser				
280		285	290	
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag				
1027				
Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu				
295		300	305	
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag				
1075				
Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys				
310		315	320	325
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				
1123				
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu				
	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				
1171				
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu				
	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				
1219				
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser				
	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				
1267				
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys				
	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				
1315				
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp				
	390	395	400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				
1363				
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly				
	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				
1411				
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly				
	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				
1459				



Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp  
 440 445 450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc  
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile  
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga

1545

Ser Thr Phe His Tyr

470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly  
 1 5 10 15

Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp  
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn  
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser  
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala  
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro  
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr  
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln  
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu  
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala  
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val  
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg  
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser  
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg  
 210 215 220

Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu  
 225 230 235 240  
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg  
 245 250 255  
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser  
 260 265 270  
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile  
 275 280 285  
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys  
 290 295 300  
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg  
 305 310 315 320  
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln  
 325 330 335  
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile  
 340 345 350  
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala  
 355 360 365  
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu  
 370 375 380  
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly  
 385 390 395 400  
 Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser  
 405 410 415  
 Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala  
 420 425 430  
 Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala  
 435 440 445  
 Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys  
 450 455 460  
 Ile Leu Ala Thr Ile Ser Thr Phe His Tyr  
 465 470

&lt;210&gt; 433

&lt;211&gt; 494

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(471)

&lt;223&gt; RXA02814

&lt;400&gt; 433

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gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc 48
Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1              5              10              15

atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
              20              25              30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
              35              40              45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
              50              55              60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
  65              70              75              80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
              85              90              95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
              100              105              110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
              115              120              125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
              130              135              140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
  145              150              155

tcttaaaaca ccg 494

```

&lt;210&gt; 434

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 434

```

Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1              5              10              15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
              20              25              30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
              35              40              45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
  50              55              60

```

His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala  
 65 70 75 80  
 Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala  
 85 90 95  
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg  
 100 105 110  
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly  
 115 120 125  
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr  
 130 135 140  
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu  
 145 150 155

<210> 435  
 <211> 803  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (1)..(780)  
 <223> RXA00229

<400> 435  
 gag gcg aaa ggc ctc gcg cag gga cgt gcg acg gtg tac agg cgc atc 48  
 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
 1 5 10 15  
 gac acg ctt ggg tcg cgt gct tcc ggg caa gat tta aat acg ctt ctc 96  
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30  
 gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144  
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45  
 tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192  
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60  
 acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240  
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80  
 acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288  
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95  
 gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336  
 Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140  
  
 gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160  
  
 gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175  
  
 aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190  
  
 gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205  
  
 ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220  
  
 acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240  
  
 cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255  
  
 ttc ctg tcc ctc taaaagagtc agtaaacct cga 803  
 Phe Leu Ser Leu  
 260

&lt;210&gt; 436

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile  
 1 5 10 15  
  
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu  
 20 25 30  
  
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro  
 35 40 45  
  
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala  
 50 55 60  
  
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His  
 65 70 75 80  
  
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu  
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala  
 100 105 110  
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val  
 115 120 125  
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu  
 130 135 140  
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val  
 145 150 155 160  
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val  
 165 170 175  
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp  
 180 185 190  
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met  
 195 200 205  
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu  
 210 215 220  
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe  
 225 230 235 240  
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr  
 245 250 255  
 Phe Leu Ser Leu  
 260

<210> 437  
 <211> 927  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(904)  
 <223> RXA02093

<400> 437  
 ggcaggaatt tcccgaaaac ttccaccaat aatcaagcca tatcccacac aatcaggcat 60  
 ttgtctttcc tttgtctcgc atgagtataa aatcactgtc atg gtc aac tac gtc 115  
 Met Val Asn Tyr Val 5  
 gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163  
 Asp Arg Glu Thr 10 Leu Cys Ile Ser 15 Ala Ala Arg Pro Ser Asn 20  
 cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211  
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn 25 30 35  
 tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

Tyr	Leu	Tyr	Lys	Ala	Val	Ala	Pro	Ala	Asp	Ile	Thr	Ala	Ala	Val	Ala		
	40						45					50					
ggt	atc	cgt	ggt	ctg	aac	att	cgc	ggc	gca	ggt	gtc	tcc	atg	cca	tac	307	
Gly	Ile	Arg	Gly	Leu	Asn	Ile	Arg	Gly	Ala	Gly	Val	Ser	Met	Pro	Tyr		
	55					60					65						
aag	agc	gat	gtc	atc	cca	ctc	atc	gat	gag	ttg	cat	cct	tcc	gca	gag	355	
Lys	Ser	Asp	Val	Ile	Pro	Leu	Ile	Asp	Glu	Leu	His	Pro	Ser	Ala	Glu		
	70				75				80					85			
cgc	ata	cgt	tct	gtt	aac	acc	atc	gtc	aac	aat	gac	gga	cac	ctt	gtc	403	
Arg	Ile	Arg	Ser	Val	Asn	Thr	Ile	Val	Asn	Asn	Asp	Gly	His	Leu	Val		
				90					95					100			
gga	tac	aac	acc	gac	tac	act	gcg	gtg	tac	cac	ctc	ctt	gaa	gaa	cac	451	
Gly	Tyr	Asn	Thr	Asp	Tyr	Thr	Ala	Val	Tyr	His	Leu	Leu	Glu	Glu	His		
			105					110					115				
cgc	gtg	aac	ccc	aat	gca	cga	gta	gct	atc	aag	gga	tcc	ggc	ggc	atg	499	
Arg	Val	Asn	Pro	Asn	Ala	Arg	Val	Ala	Ile	Lys	Gly	Ser	Gly	Gly	Met		
		120					125					130					
gcc	aat	gct	gtt	gtt	gca	gct	ctt	gct	gag	tat	ggt	ctg	agt	ggc	acc	547	
Ala	Asn	Ala	Val	Val	Ala	Ala	Leu	Ala	Glu	Tyr	Gly	Leu	Ser	Gly	Thr		
	135					140					145						
gtc	gtt	gcc	cgc	aac	cac	acc	acc	ggt	tct	gcg	cta	gct	tcc	cgt	tac	595	
Val	Val	Ala	Arg	Asn	His	Thr	Thr	Gly	Ser	Ala	Leu	Ala	Ser	Arg	Tyr		
	150				155					160					165		
ggt	tgg	gaa	tac	tcc	gca	act	gtt	ccg	gaa	gac	gca	aaa	att	ttg	gtt	643	
Gly	Trp	Glu	Tyr	Ser	Ala	Thr	Val	Pro	Glu	Asp	Ala	Lys	Ile	Leu	Val		
				170					175					180			
aat	gta	acc	cca	atg	gga	atg	aat	gga	cct	gac	caa	gac	gtt	gta	tct	691	
Asn	Val	Thr	Pro	Met	Gly	Met	Asn	Gly	Pro	Asp	Gln	Asp	Val	Val	Ser		
			185					190					195				
ttt	ggt	gag	gat	gaa	gta	gac	cga	gcc	gac	gta	atc	ttt	gac	tgc	gta	739	
Phe	Gly	Glu	Asp	Glu	Val	Asp	Arg	Ala	Asp	Val	Ile	Phe	Asp	Cys	Val		
		200					205					210					
gca	ttc	ccc	gtc	gag	acc	cca	ctg	att	aag	ttg	gcc	aag	gaa	aag	ggt	787	
Ala	Phe	Pro	Val	Glu	Thr	Pro	Leu	Ile	Lys	Leu	Ala	Lys	Glu	Lys	Gly		
	215					220					225						
aag	caa	acc	atc	gac	ggc	gga	gaa	gtt	gcc	gct	ctt	cag	gca	gca	gag	835	
Lys	Gln	Thr	Ile	Asp	Gly	Gly	Glu	Val	Ala	Ala	Leu	Gln	Ala	Ala	Glu		
	230				235				240						245		
cag	ttc	cac	ctc	tac	acc	gga	gtt	ctt	cca	acc	aac	gac	cag	atc	att	883	
Gln	Phe	His	Leu	Tyr	Thr	Gly	Val	Leu	Pro	Thr	Asn	Asp	Gln	Ile	Ile		
				250				255						260			
gct	gcg	gag	gag	ttc	tcc	aag	taaattttctc	tcccctatttt	tta							927	
Ala	Ala	Glu	Glu	Phe	Ser	Lys											
				265													

&lt;210&gt; 438

&lt;211&gt; 268

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 438

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Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala
  1              5              10              15

Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala
      20              25              30

Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile
      35              40              45

Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly
      50              55              60

Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu
      65              70              75              80

His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn
      85              90              95

Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His
      100             105             110

Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys
      115             120             125

Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr
      130             135             140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala
      145             150             155             160

Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp
      165             170             175

Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp
      180             185             190

Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val
      195             200             205

Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu
      210             215             220

Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala
      225             230             235             240

Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr
      245             250             255

Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys
      260             265

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&lt;210&gt; 439

&lt;211&gt; 951

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(928)

&lt;223&gt; RXA02791

&lt;400&gt; 439

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accgtgttca acgacacctt cgaagagcac gaagccgaca ttgagcaagc tttgaacagt 60

ggcgttctag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115
                                   Leu Gly Ser His Ile
                                   1 5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
                                   10 15 20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
                                   25 30 35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
                                   40 45 50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
                                   55 60 65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
                                   70 75 80 85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
                                   90 95 100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
                                   105 110 115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
                                   120 125 130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
                                   135 140 145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
                                   150 155 160 165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
                                   170 175 180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
                                   185 190 195

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gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739  
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp  
           200                          205                          210

gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787  
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala  
           215                          220                          225

aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835  
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser  
           230                          235                          240                          245

tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883  
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala  
                           250                          255                          260

atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928  
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His  
                           265                          270                          275

taagtcctccg ccacctcctc aac 951

<210> 440  
 <211> 276  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 440  
 Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile  
   1                          5                          10                          15

Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu  
           20                          25                          30

Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met  
           35                          40                          45

Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser  
           50                          55                          60

Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val  
           65                          70                          75                          80

Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr  
                           85                          90                          95

Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly  
           100                          105                          110

Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala  
           115                          120                          125

Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu  
           130                          135                          140

Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg  
           145                          150                          155                          160

Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala  
                           165                          170                          175

Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser  
 180 185 190  
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile  
 195 200 205  
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val  
 210 215 220  
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met  
 225 230 235 240  
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp  
 245 250 255  
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile  
 260 265 270  
 Ser Glu Glu His  
 275

<210> 441  
 <211> 693  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(670)  
 <223> RXA01699

<400> 441  
 ctgcagaaat tcggcgggtga ctccctgagc gaaaccaaga gcaacattga cacctacctc 60  
 aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115  
 Met Glu Arg Asn Glu  
 1 5  
 gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163  
 Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu  
 10 15 20  
 tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211  
 Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys  
 25 30 35  
 tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259  
 Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val  
 40 45 50  
 gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307  
 Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala  
 55 60 65  
 gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355  
 Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile  
 70 75 80 85  
 cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403

His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly  
                             90                            95                            100

gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451  
 Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp  
                             105                            110                            115

gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499  
 Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala  
                             120                            125                            130

aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547  
 Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His  
                             135                            140                            145

tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595  
 Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala  
                             150                            155                            160                            165

acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643  
 Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala  
                             170                            175                            180

gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690  
 Ala Val Leu His His Leu Glu Ile Asp  
                             185                            190

tta 693

&lt;210&gt; 442

&lt;211&gt; 190

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 442

Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser  
   1                            5                            10                            15

Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu  
                             20                            25                            30

Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu  
                             35                            40                            45

Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly  
                             50                            55                            60

Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg  
                             65                            70                            75                            80

Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val  
                             85                            90                            95

Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu  
                             100                            105                            110

Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly  
                             115                            120                            125

Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala

130	135	140	
Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu 145 150 155 160			
Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro 165 170 175			
Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp 180 185 190			
<210> 443			
<211> 959			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (97)..(936)			
<223> RXA00952			
<400> 443			
catcctcgtc tccctatccg gccgtggcga caaggacgtt gaccacgtgc gccgcaccct 60			
cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat 114			
		Met Ser Arg Tyr Asp Asp	
		1 5	
ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc 162			
Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe			
	10	15	20
atc atg ctg agc gac cct tca cca gag gag gct ttc cag atc atc tcc 210			
Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser			
	25	30	35
aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc 258			
Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe			
	40	45	50
tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc 306			
Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg			
	55	60	70
gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag 354			
Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys			
	75	80	85
cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac 402			
Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr			
	90	95	100
ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc 450			
Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe			
	105	110	115
gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga 498			
Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg			
	120	125	130

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546  
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Gly Ile Asp Pro  
 135 140 145 150  
 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594  
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val  
 155 160 165  
 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642  
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val  
 170 175 180  
 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690  
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val  
 185 190 195  
 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738  
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly  
 200 205 210  
 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786  
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser  
 215 220 225 230  
 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834  
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys  
 235 240 245  
 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882  
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu  
 250 255 260  
 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930  
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys  
 265 270 275  
 aag gtt taggccttta aatgtggcaa tgt 959  
 Lys Val  
 280

&lt;210&gt; 444

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 444

Met Ser Arg Tyr Asp Asp Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu  
 1 5 10 15  
 Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu  
 20 25 30  
 Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu  
 35 40 45  
 Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val  
 50 55 60  
 Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser  
 65 70 75 80

Ala Leu Glu Gln Ile Lys Arg Val Arg Ala Ala Tyr Pro Glu Val Pro  
85 90 95

Ile Gly Met Leu Ile Tyr Gly Asn Val Pro Phe Thr Arg Gly Leu Asp  
100 105 110

Arg Phe Tyr Gln Glu Phe Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu  
115 120 125

Pro Asp Val Pro Val Arg Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala  
130 135 140

Ala Ala Gly Ile Asp Pro Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu  
145 150 155 160

Lys Thr Leu Glu Gly Val Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala  
165 170 175

Ile Ser Arg Asp Gly Val Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp  
180 185 190

Gly Leu Ser Ala Val Val Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro  
195 200 205

Ile Leu Leu Gly Phe Gly Ile Ser Ser Pro Gln His Val Ala Asp Ala  
210 215 220

Ile Ala Ala Gly Ala Ser Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys  
225 230 235 240

Ile Ile Ala Ser His Cys Glu Gly Glu His Pro Asn Pro Ser Thr Ile  
245 250 255

Arg Asp Met Asp Gly Leu Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala  
260 265 270

Met Lys Ala Ala Thr Lys Lys Val  
275 280

&lt;210&gt; 445

&lt;211&gt; 1237

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1237)

&lt;223&gt; RXN00956

&lt;400&gt; 445

gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaagggttt aaataggatc atg act gaa aaa gaa 115  
Met Thr Glu Lys Glu  
1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	



gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931  
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly  
                   265                                   270                                   275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979  
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly  
                   280                                   285                                   290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc  
 1027  
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser  
                   295                                   300                                   305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac  
 1075  
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His  
 310                                   315                                   320                                   325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac  
 1123  
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp  
                   330                                   335                                   340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc  
 1171  
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile  
                   345                                   350                                   355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc  
 1219  
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg  
                   360                                   365                                   370

gcc aag acc gcc gaa gta  
 1237  
 Ala Lys Thr Ala Glu Val  
                   375

<210> 446

<211> 379

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 446

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr  
           1                                   5                                   10                                   15

Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala  
                   20                                   25                                   30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
                   35                                   40                                   45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
                   50                                   55                                   60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
                   65                                   70                                   75                                   80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

85										90					95				
Ala	His	Lys	Thr	Asn	Gln	Val	Ile	Gly	Gln	Val	Leu	Leu	Ala	Lys	Arg				
			100					105					110						
Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly				
		115					120					125							
Thr	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val				
	130					135					140								
Tyr	Met	Gly	Ala	Lys	Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg				
145					150					155					160				
Met	Gln	Leu	His	Gly	Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly				
				165					170					175					
Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr				
			180					185					190						
Phe	His	Glu	Ser	His	Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro				
	195					200						205							
Phe	Pro	Thr	Ile	Val	Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala				
	210					215					220								
Lys	Ala	Gln	Met	Leu	Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val				
225					230					235					240				
Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe				
				245					250					255					
Ile	Asp	Asp	Glu	Gly	Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu				
			260					265					270						
Gly	Leu	Asp	Ser	Gly	Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile				
	275						280					285							
Gly	Ile	Leu	His	Gly	Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly				
	290					295					300								
Gln	Val	Glu	Glu	Ser	Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly				
305					310					315					320				
Val	Gly	Pro	Gln	His	Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr				
				325					330					335					
Val	Gly	Ile	Thr	Asp	Ala	Glu	Ala	Leu	Gln	Ala	Phe	Gln	Tyr	Leu	Ala				
			340					345					350						
Arg	Tyr	Glu	Gly	Ile	Ile	Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Phe	Ala				
		355					360					365							
Tyr	Ala	Leu	Lys	Arg	Ala	Lys	Thr	Ala	Glu	Val									
	370					375													

&lt;210&gt; 447

&lt;211&gt; 1231

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1231)

&lt;223&gt; FRXA00956

&lt;400&gt; 447

gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaagggttt aaataggatc atg act gaa aaa gaa 115  
 Met Thr Glu Lys Glu  
 1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163  
 Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly  
 10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211  
 Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu  
 25 30 35

aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259  
 Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu  
 40 45 50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307  
 Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu  
 55 60 65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355  
 Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile  
 70 75 80 85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403  
 Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn  
 90 95 100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451  
 Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg  
 105 110 115

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499  
 Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu  
 120 125 130

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547  
 Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys  
 135 140 145

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595  
 Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly  
 150 155 160 165

gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643  
 Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala  
 170 175 180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691  
 Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His  
 185 190 195

```

tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg 739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val
      200      205      210

cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta 787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu
      215      220      225

gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt 835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly
      230      235      240      245

ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt 883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly
      250      255      260

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc gcc 931
Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
      265      270      275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac gcc 979
Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
      280      285      290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc
1027
Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
      295      300      305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac
1075
Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
      310      315      320      325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac
1123
Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
      330      335      340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc
1171
Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
      345      350      355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc
1219
Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
      360      365      370

gcc aag acc gcc
1231
Ala Lys Thr Ala
      375

```

&lt;210&gt; 448

&lt;211&gt; 377

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 448

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr  
 1 5 10 15  
 Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala  
 20 25 30  
 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu  
 35 40 45  
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro  
 50 55 60  
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys  
 65 70 75 80  
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly  
 85 90 95  
 Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg  
 100 105 110  
 Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly  
 115 120 125  
 Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val  
 130 135 140  
 Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg  
 145 150 155 160  
 Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly  
 165 170 175  
 Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr  
 180 185 190  
 Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro  
 195 200 205  
 Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala  
 210 215 220  
 Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val  
 225 230 235 240  
 Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe  
 245 250 255  
 Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu  
 260 265 270  
 Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile  
 275 280 285  
 Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly  
 290 295 300  
 Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly  
 305 310 315 320  
 Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr

657

aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg 547  
Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr  
135 140 145

gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc 595  
Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly  
150 155 160 165

cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag 643  
Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys  
170 175 180

ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg 691  
Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val  
185 190 195

aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg 739  
Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro  
200 205 210

gac ttc cgc gtt gtg tgg gat aat gcc tac gcc gtt cat acg ctg acc 787  
Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr  
215 220 225

gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct 835  
Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala  
230 235 240 245

ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act 883  
Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr  
250 255 260

ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc 931  
Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg  
265 270 275

aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag 979  
Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys  
280 285 290

gtc aat cag ttg gct cat gcg cgt tac ttt ggc gat gct gag gga gtg  
1027  
Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val  
295 300 305

cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac  
1075  
Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn  
310 315 320 325

aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg  
1123  
Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala  
330 335 340

cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt  
1171  
Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val  
345 350 355

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc  
 1219  
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile  
           360                                  365                                  370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag  
 1267  
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu  
           375                                  380                                  385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt  
 1315  
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu  
 390                                  395                                  400                                  405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg  
 1363  
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala  
                                   410                                  415                                  420

gag cat tac gct aac taaaagtgaac tacagcggag aca  
 1401  
 Glu His Tyr Ala Asn  
                                   425

<210> 450

<211> 426

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 450

Met Ser Ser Val Ser Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu  
   1                                  5                                  10                                  15

Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn  
                                   20                                  25                                  30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp  
                                   35                                  40                                  45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala  
                                   50                                  55                                  60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val  
                                   65                                  70                                  75                                  80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln  
                                   85                                  90                                  95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile  
                                   100                                  105                                  110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser  
                                   115                                  120                                  125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg  
                                   130                                  135                                  140

His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro  
                                   145                                  150                                  155                                  160



Met Asn Glu Asp Gly Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys  
 165 170 175  
 Asn Pro Gln Val Lys Gly Met Trp Val Val Pro Val Phe Ser Asn Pro  
 180 185 190  
 Thr Gly Phe Thr Val Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met  
 195 200 205  
 Glu Thr Ala Ala Pro Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala  
 210 215 220  
 Val His Thr Leu Thr Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly  
 225 230 235 240  
 Leu Gly Glu Ala Ala Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser  
 245 250 255  
 Thr Ser Lys Ile Thr Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr  
 260 265 270  
 Ser Ala Glu Asn Arg Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly  
 275 280 285  
 Ile Gly Pro Asn Lys Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly  
 290 295 300  
 Asp Ala Glu Gly Val Arg Ala Val Met Arg Lys His Ala Ala Ser Leu  
 305 310 315 320  
 Ala Pro Lys Phe Asn Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala  
 325 330 335  
 Glu Tyr Gly Val Ala Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile  
 340 345 350  
 Ser Leu Asp Val Val Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala  
 355 360 365  
 Lys Glu Ala Gly Ile Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu  
 370 375 380  
 Arg Gln Asp Pro Glu Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro  
 385 390 395 400  
 Pro Val Glu Glu Leu Glu Val Ala Met Asp Gly Val Ala Thr Cys Val  
 405 410 415  
 Leu Leu Ala Ala Ala Glu His Tyr Ala Asn  
 420 425

&lt;210&gt; 451

&lt;211&gt; 1143

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1120)

&lt;223&gt; RXN00448

&lt;400&gt; 451

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ccattttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtggt 60
catagagata accgtagtag gtatgtgccca cacttggtcag gtg act acc aaa gac 115
                               Val Thr Thr Lys Asp
                               1                               5
att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                               10                               15                               20
ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                               25                               30                               35
cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                               40                               45                               50
tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                               55                               60                               65
ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg ctt ctc gac 355
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser Leu Leu Asp
                               70                               75                               80                               85
gcc gtc cac acc cac gca cca aac aac ggc ttc acc gac gtc gta tcc 403
Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser
                               90                               95                               100
gta aaa acc gcc gtc tac gac gca gta aaa gcc cgc aac atg caa cac 451
Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His
                               105                               110                               115
cgt tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg 499
Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp
                               120                               125                               130
agc gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc 547
Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr
                               135                               140                               145
ttc gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc 595
Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser
                               150                               155                               160                               165
atc tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt 643
Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val
                               170                               175                               180
gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691
Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
                               185                               190                               195
cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
                               200                               205                               210

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ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787  
 Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser  
 215 220 225

acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835  
 Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala M t Cys Glu  
 230 235 240 245

agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883  
 Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile  
 250 255 260

ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931  
 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu  
 265 270 275

caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979  
 Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg  
 280 285 290

tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca  
 1027  
 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser  
 295 300 305

tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag  
 1075  
 Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys  
 310 315 320 325

cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc  
 1120  
 Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe  
 330 335 340

tagttttatc ggctgatgat tct  
 1143

&lt;210&gt; 452

&lt;211&gt; 340

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 452

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly  
 1 5 10 15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser  
 20 25 30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp  
 35 40 45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala  
 50 55 60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile  
 65 70 75 80

Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe

85					90					95					
Thr	Asp	Val	Val	Ser	Val	Lys	Thr	Ala	Val	Tyr	Asp	Ala	Val	Lys	Ala
		100						105					110		
Arg	Asn	Met	Gln	His	Arg	Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr
		115					120					125			
Ala	Asn	Ser	Gly	Trp	Ser	Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala
		130					135					140			
Val	Trp	Val	Val	Thr	Phe	Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn
		145				150					155				160
Ser	Thr	Trp	Ile	Ser	Ile	Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala
			165					170						175	
Val	Gly	Ala	Glu	Val	Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala
			180					185					190		
Ala	Ala	Arg	Val	Ser	His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala
		195					200					205			
Ile	Val	Gly	Asp	Asn	Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly
		210				215					220				
Ser	Tyr	Arg	Asp	Ser	Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val
		225				230					235				240
Arg	Ala	Met	Cys	Glu	Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp
			245					250						255	
Glu	Ala	Leu	Ala	Ile	Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu
			260					265					270		
Gln	Pro	Asn	Ile	Glu	Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile
		275					280					285			
Arg	Tyr	Glu	Ala	Arg	Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser
		290				295					300				
Pro	Thr	Ile	Thr	Ser	Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr
		305				310					315				320
Pro	Asn	Trp	Glu	Lys	Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg
			325						330					335	
Ile	Glu	Val	Phe												
			340												

&lt;210&gt; 453

&lt;211&gt; 689

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(666)

&lt;223&gt; FRXA00448

&lt;400&gt; 453

tat	gtg	gga	tcc	cac	ccc	atg	gca	ggc	acc	gcc	aac	tcc	ggc	tgg	agc	48
Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr	Ala	Asn	Ser	Gly	Trp	Ser	
1				5					10					15		
gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc	96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe	
			20				25						30			
gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc	144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile	
		35					40					45				
tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc	192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val	
	50					55					60					
cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat	240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His	
	65				70					75					80	
tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggc	gac	aac	ggc	288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly	
			85						90					95		
ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc	336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr	
			100				105						110			
cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc	384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser	
		115					120					125				
aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc	432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu	
	130					135					140					
cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa	480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln	
	145				150					155					160	
ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc	528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser	
			165						170					175		
ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc	576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser	
			180					185					190			
agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag	624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln	
		195					200					205				
ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc			666
Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe			
	210					215					220					
tag	ttttatc	ggctgatgat	tct													689

&lt;210&gt; 454

&lt;211&gt; 222

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 454

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Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser
 1              5              10              15

Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe
      20              25              30

Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
      35              40              45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
      50              55              60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His
      65              70              75              80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
      85              90              95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
      100              105              110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
      115              120              125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
      130              135              140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
      145              150              155              160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
      165              170              175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
      180              185              190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
      195              200              205

Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
      210              215              220

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&lt;210&gt; 455

&lt;211&gt; 346

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(346)

&lt;223&gt; FRXA00452

&lt;400&gt; 455

ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtgtt 60

catagagata accgtagtag gtatgtgccca cacttgtcag gtg act acc aaa gac 115  
Val Thr Thr Lys Asp  
1 5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163  
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser  
10 15 20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211  
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn  
25 30 35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259  
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val  
40 45 50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307  
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala  
55 60 65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346  
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser  
70 75 80

&lt;210&gt; 456

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 456

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly  
1 5 10 15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser  
20 25 30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp  
35 40 45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala  
50 55 60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile  
65 70 75 80

Asp Ser

&lt;210&gt; 457

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1225)

&lt;223&gt; RXA00584

&lt;400&gt; 457

tagttgtgcc acctaaaacg cgaacagaac cggagtcgag cagcacctcc ccgcaagggt 60

agaggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa 115  
Met His Ser Pro Glu  
1 5

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163  
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser  
10 15 20

acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211  
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr  
25 30 35

gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259  
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val  
40 45 50

gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307  
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp  
55 60 65

cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355  
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala  
70 75 80 85

gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403  
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp  
90 95 100

cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451  
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr  
105 110 115

atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499  
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr  
120 125 130

tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547  
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp  
135 140 145

gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac 595  
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn  
150 155 160 165

agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct 643  
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala  
170 175 180

cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct 691  
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser  
185 190 195

atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca 739  
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala  
200 205 210

gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc 787  
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr  
215 220 225



tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835  
 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn  
 230 235 240 245

tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883  
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala  
 250 255 260

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931  
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu  
 265 270 275

atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979  
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln  
 280 285 290

gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa  
 1027  
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu  
 295 300 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag  
 1075  
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln  
 310 315 320 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg  
 1123  
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val  
 330 335 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc  
 1171  
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile  
 345 350 355

gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca  
 1219  
 Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala  
 360 365 370

gcc aag taattaaggg cgctagactg tta  
 1248  
 Ala Lys  
 375

<210> 458

<211> 375

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 458

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu  
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Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu  
 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys

35					40					45					
Gln	Ala	Ser	Lys	Val	Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe
50					55					60					
Ala	Gly	Asp	Asp	Asp	Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val
65					70					75					80
His	Asp	Pro	Glu	Ala	Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu
				85					90					95	
Ala	Lys	Arg	Leu	Asp	Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe
			100					105					110		
Glu	Lys	Pro	Arg	Thr	Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro
		115					120					125			
His	Leu	Asn	Glu	Thr	Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg
	130					135					140				
Lys	Val	Leu	Ile	Asp	Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu
145				150						155					160
Phe	Leu	Glu	Pro	Asn	Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp
				165					170					175	
Gly	Ala	Ile	Gly	Ala	Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu
			180					185					190		
Ala	Ser	Gly	Met	Ser	Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly
		195					200					205			
Asn	Ile	Gln	Val	Ala	Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His
	210					215					220				
Phe	Phe	Phe	Gly	Thr	Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr
225				230						235				240	
Ala	Gly	Asn	Ser	Asn	Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly
				245					250					255	
Pro	Asn	His	Asp	Ala	Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly
			260					265					270		
Glu	Asn	Ala	Arg	Leu	Met	Ile	Asp	Ala	Ser	His	Ala	Asn	Ser	Gly	Lys
		275					280					285			
Asp	His	Ile	Arg	Gln	Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile
	290					295					300				
Ser	Gly	Gly	Ser	Glu	Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu
305				310					315						320
Val	Gly	Gly	Ala	Gln	Asn	Leu	Asp	Pro	Ala	Lys	Leu	Arg	Ile	Asn	Gly
				325					330					335	
Gly	Glu	Gly	Leu	Val	Tyr	Gly	Gln	Ser	Val	Thr	Asp	Lys	Cys	Ile	Asp
			340					345					350		
Ile	Asp	Thr	Thr	Ile	Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg
		355				360					365				

Glu Arg Arg Ala Ala Ala Lys  
370 375

<210> 459

<211> 1983

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1960)

<223> RXA00579

<400> 459

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                                         Met Arg Val Leu Ile
                                         1 5

att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
                        10 15 20

gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
                        25 30 35

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
                        40 45 50

gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg
                        55 60 65

gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
                        70 75 80 85

ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly
                        90 95 100

gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
                        105 110 115

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
                        120 125 130

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
                        135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His
                        150 155 160 165

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ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc	643
Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe	
170 175 180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att	691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile	
185 190 195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat	739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His	
200 205 210	
tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt	787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu	
215 220 225	
ggg gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc	835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly	
230 235 240 245	
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca	883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser	
250 255 260	
gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt	931
Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly	
265 270 275	
tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt	979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser	
280 285 290	
ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa	
1027	
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu	
295 300 305	
tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt	
1075	
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe	
310 315 320 325	
gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct	
1123	
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro	
330 335 340	
gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat	
1171	
Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr	
345 350 355	
ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg	
1219	
Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser	
360 365 370	
tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc	
1267	
Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala	

375	380	385
cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat 1315		
Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr 390 395 400 405		
ggg gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg 1363		
Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro 410 415 420		
gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc 1411		
Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro 425 430 435		
att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa 1459		
Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu 440 445 450		
atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg 1507		
Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu 455 460 465		
atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc 1555		
Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro 470 475 480 485		
acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca 1603		
Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr 490 495 500		
gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt 1651		
Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser 505 510 515		
ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt 1699		
Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly 520 525 530		
gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct 1747		
Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala 535 540 545		
cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc 1795		
Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly 550 555 560 565		
gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat 1843		
Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn 570 575 580		

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg  
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro  
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat  
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn  
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt  
1983

Leu Phe Gly Val Glu Phe Pro  
615 620

<210> 460

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu  
1 5 10 15

Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro  
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser  
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala  
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly  
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro  
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly  
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser  
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser  
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp  
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln  
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu  
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu  
195 200 205

Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln  
 210 215 220  
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys  
 225 230 235 240  
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp  
 245 250 255  
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp  
 260 265 270  
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala  
 275 280 285  
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg  
 290 295 300  
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu  
 305 310 315 320  
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val  
 325 330 335  
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp  
 340 345 350  
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile  
 355 360 365  
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly  
 370 375 380  
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala  
 385 390 395 400  
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile  
 405 410 415  
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr  
 420 425 430  
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala  
 435 440 445  
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp  
 450 455 460  
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala  
 465 470 475 480  
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val  
 485 490 495  
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu  
 500 505 510  
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly  
 515 520 525

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp  
 530 535 540

Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr  
 545 550 555 560

Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu  
 565 570 575

Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu  
 580 585 590

Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser  
 595 600 605

Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro  
 610 615 620

<210> 461  
 <211> 747  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(724)  
 <223> RXA00958

<400> 461  
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ccattgcgct tgctgctggg tccactttgg aggtcatccg atg aca cac gtt gtt 115  
 Met Thr His Val Val  
 1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163  
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe  
 10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211  
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val  
 25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259  
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly  
 40 45 50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307  
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg  
 55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355  
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala  
 70 75 80 85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403  
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His  
 90 95 100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451



Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro  
 105 110 115  
 gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499  
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile  
 120 125 130  
 cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547  
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val  
 135 140 145  
 gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595  
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile  
 150 155 160 165  
 ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643  
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly  
 170 175 180  
 ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691  
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile  
 185 190 195  
 ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaaa aggatttgat 744  
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn  
 200 205  
 tca 747

&lt;210&gt; 462

&lt;211&gt; 208

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 462

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn  
 1 5 10 15  
 Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg  
 20 25 30  
 Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile  
 35 40 45  
 Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met  
 50 55 60  
 Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys  
 65 70 75 80  
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro  
 85 90 95  
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala  
 100 105 110  
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro  
 115 120 125  
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His

130	135	140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr		
145	150	155
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp		
	165	170
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro		
	180	185
Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn		
	195	200
		205

<210> 463  
 <211> 469  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(469)  
 <223> RXN03007

<400> 463  
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 gaacagcttc tcgcgaacta ataaaaaaag gattttgattc atg act tct cca gca 115  
 Met Thr Ser Pro Ala  
 1 5  
 aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg 163  
 Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu  
 10 15 20  
 gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat 211  
 Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp  
 25 30 35  
 gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag 259  
 Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu  
 40 45 50  
 cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct 307  
 Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala  
 55 60 65  
 cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act 355  
 Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr  
 70 75 80 85  
 ggt ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg 403  
 Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu  
 90 95 100  
 atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg 451  
 Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser

105 110 115

gtg agc tcc aag tcc ggc 469  
Val Ser Ser Lys Ser Gly  
120

<210> 464  
<211> 123  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 464  
Met Thr Ser Pro Ala Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn  
1 5 10 15  
Pro Thr Pro Thr Leu Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr  
20 25 30  
Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile  
35 40 45  
Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala  
50 55 60  
Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu  
65 70 75 80  
Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr  
85 90 95  
Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys  
100 105 110  
His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly  
115 120

<210> 465  
<211> 564  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101)..(541)  
<223> RXN02918

<400> 465  
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tgattctatt attgccaaat cagaaagcag gagagacccg atg agc gaa atc cta 115  
Met Ser Glu Ile Leu  
1 5  
gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163  
Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala  
10 15 20  
ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211  
Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His

25										30										35										
acc	ctg	ttc	ggg	gat	tta	ggt	tta	gac	gga	ctc	tct	gga	aac	tac	acc	259														
Thr	Leu	Phe	Gly	Asp	Leu	Gly	Leu	Asp	Gly	Leu	Ser	Gly	Asn	Tyr	Thr															
40						45						50																		
gac	act	gag	att	gac	ggc	tac	ggc	gac	gca	ttc	ctg	ctg	gtt	gca	gcg	307														
Asp	Thr	Glu	Ile	Asp	Gly	Tyr	Gly	Asp	Ala	Phe	Leu	Leu	Val	Ala	Ala															
55			60						65																					
cta	tcc	gtg	ttg	atg	gct	gaa	aac	aaa	gca	aca	ggt	ggc	gtg	aat	ctg	355														
Leu	Ser	Val	Leu	Met	Ala	Glu	Asn	Lys	Ala	Thr	Gly	Gly	Val	Asn	Leu															
70				75				80				85																		
ggt	gag	ctt	ggg	gga	gct	gat	aaa	tcg	atc	cgg	ctg	cat	gtt	gaa	tcc	403														
Gly	Glu	Leu	Gly	Gly	Ala	Asp	Lys	Ser	Ile	Arg	Leu	His	Val	Glu	Ser															
			90						95			100																		
aag	gag	aac	acc	caa	atc	aac	acc	gca	ttg	aag	tat	ttt	gcg	ctc	tcc	451														
Lys	Glu	Asn	Thr	Gln	Ile	Asn	Thr	Ala	Leu	Lys	Tyr	Phe	Ala	Leu	Ser															
			105						110			115																		
cca	gaa	gac	cac	gca	gca	gca	gat	cgc	ttc	gat	gag	gat	gac	ctg	tct	499														
Pro	Glu	Asp	His	Ala	Ala	Ala	Asp	Arg	Phe	Asp	Glu	Asp	Asp	Leu	Ser															
120						125						130																		
gag	ctt	gcc	aac	ttg	agt	gaa	gag	ctg	cgc	gga	cag	ctg	gac			541														
Glu	Leu	Ala	Asn	Leu	Ser	Glu	Glu	Leu	Arg	Gly	Gln	Leu	Asp																	
135				140				145																						
taattgtctc ccatttaagg agt															564															

&lt;210&gt; 466

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 466

Met	Ser	Glu	Ile	Leu	Glu	Thr	Tyr	Trp	Ala	Pro	His	Phe	Gly	Lys	Thr
1				5					10					15	
Glu	Glu	Ala	Thr	Ala	Leu	Val	Ser	Tyr	Leu	Ala	Gln	Ala	Ser	Gly	Asp
			20					25					30		
Pro	Ile	Glu	Val	His	Thr	Leu	Phe	Gly	Asp	Leu	Gly	Leu	Asp	Gly	Leu
			35				40					45			
Ser	Gly	Asn	Tyr	Thr	Asp	Thr	Glu	Ile	Asp	Gly	Tyr	Gly	Asp	Ala	Phe
	50					55					60				
Leu	Leu	Val	Ala	Ala	Leu	Ser	Val	Leu	Met	Ala	Glu	Asn	Lys	Ala	Thr
65					70					75					80
Gly	Gly	Val	Asn	Leu	Gly	Glu	Leu	Gly	Gly	Ala	Asp	Lys	Ser	Ile	Arg
			85					90						95	
Leu	His	Val	Glu	Ser	Lys	Glu	Asn	Thr	Gln	Ile	Asn	Thr	Ala	Leu	Lys
			100					105					110		
Tyr	Phe	Ala	Leu	Ser	Pro	Glu	Asp	His	Ala	Ala	Ala	Asp	Arg	Phe	Asp

115	120	125	
Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser		Glu Glu Leu Arg Gly	
130	135	140	
Gln Leu Asp			
145			
<210> 467			
<211> 735			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(712)			
<223> RXN01116			
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acaggacggt gtctaactaa tgacttggga tcataaccaa atg gca gcc cgc gtt	115		
	Met Ala Ala Arg Val		
	1 5		
gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg	163		
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met			
	10 15 20		
cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt	211		
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu			
	25 30 35		
cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag	259		
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu			
	40 45 50		
gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt	307		
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val			
	55 60 65		
gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc	355		
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile			
	70 75 80 85		
cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc	403		
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser			
	90 95 100		
cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag	451		
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys			
	105 110 115		
ggt atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc	499		
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile			
	120 125 130		
gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag	547		
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys			
	135 140 145		

gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595  
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val  
 150 155 160 165  
 acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc 643  
 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu  
 170 175 180  
 atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691  
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr  
 185 190 195  
 gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735  
 Glu Ala Asp Phe Lys Val Ala  
 200

&lt;210&gt; 468

&lt;211&gt; 204

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 468

Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn  
 1 5 10 15  
 Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly  
 20 25 30  
 Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro  
 35 40 45  
 Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys  
 50 55 60  
 Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp  
 65 70 75 80  
 Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly  
 85 90 95  
 Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro  
 100 105 110  
 Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly  
 115 120 125  
 Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala  
 130 135 140  
 Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys  
 145 150 155 160  
 Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu  
 165 170 175  
 Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu  
 180 185 190  
 Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

195

200

<210> 469  
 <211> 876  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101) .. (853)  
 <223> RXN01115

<400> 469  
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gccaggggtct tgcagctgtc tttgaaaagg agaactaaaa atg gct att ttg cac 115  
 Met Ala Ile Leu His  
 1 5

agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tgc 163  
 Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser  
 10 15 20

ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat 211  
 Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His  
 25 30 35

aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259  
 Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser  
 40 45 50

gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307  
 Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val  
 55 60 65

ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga 355  
 Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly  
 70 75 80 85

cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403  
 Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp  
 90 95 100

cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451  
 Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu  
 105 110 115

ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499  
 Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr  
 120 125 130

ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547  
 Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp  
 135 140 145

ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc 595  
 Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala  
 150 155 160 165

ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643

Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr  
 170 175 180  
 tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc 691  
 Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr  
 185 190 195  
 atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc 739  
 Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile  
 200 205 210  
 att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca 787  
 Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro  
 215 220 225  
 gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg 835  
 Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu  
 230 235 240 245  
 cta gca cag cat ttc gct taatgttgta ggcatgttca caa 876  
 Leu Ala Gln His Phe Ala  
 250

&lt;210&gt; 470

&lt;211&gt; 251

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 470

Met Ala Ile Leu His Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu  
 1 5 10 15  
 Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln  
 20 25 30  
 Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg  
 35 40 45  
 Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp  
 50 55 60  
 Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn  
 65 70 75 80  
 Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu  
 85 90 95  
 Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala  
 100 105 110  
 Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys  
 115 120 125  
 Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp  
 130 135 140  
 Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe  
 145 150 155 160  
 Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys



	165		170		175
Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr					
	180		185		190
Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro					
	195		200		205
Ala Thr Val Gln Ile Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala					
	210		215		220
Glu Val Leu Ser Pro Ala Ala His Val Pro Thr Val Glu Arg Pro Asn					
	225		230		235
Glu Val Asn Glu Leu Leu Ala Gln His Phe Ala					
	245		250		

&lt;210&gt; 471

&lt;211&gt; 1284

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1261)

&lt;223&gt; RXS00116

&lt;400&gt; 471

cgcggcacgc acgctggggg caagcgtcga caagcacaaa ctttttgctt aattgaatcc 60

tttgcgcacc aatcaatggg ggatcaaata tagtagctgc	atg agt aat gac ttc	115
	Met Ser Asn Asp Phe	
	1 5	

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg	163
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met	
	10 15 20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt	211
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe	
	25 30 35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag	259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln	
	40 45 50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg	307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser	
	55 60 65

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag	355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu	
	70 75 80 85

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg	403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala	
	90 95 100

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc	451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile	

105	110	115	
gtt ttg gaa ccg tat tac gat gcg	tat gcg gcg gct att gcg ttg gcg	499	
Val Leu Glu Pro Tyr Tyr Asp Ala	Tyr Ala Ala Ala Ile Ala Leu Ala		
120	125 130		
ggg gcg acg cgg gtg gcg gtt cct	ttg cag gag gtg gag aac tcg tgg	547	
Gly Ala Thr Arg Val Ala Val Pro	Leu Gln Glu Val Glu Asn Ser Trp		
135	140 145		
gat gtg gat gtc gat aag ttg cat	gcg gcg gtg act aag aag acg cgg	595	
Asp Val Asp Val Asp Lys Leu His	Ala Ala Val Thr Lys Lys Thr Arg		
150	155 160 165		
atg att atc gtt aat tcg ccg cat	aat ccg acg ggt tcg gtg ttt tct	643	
Met Ile Ile Val Asn Ser Pro His	Asn Pro Thr Gly Ser Val Phe Ser		
170	175 180		
aag aag gcg ttg aag cag ttg gcg	ggt gtt gct cgt gcg tat gac ttg	691	
Lys Lys Ala Leu Lys Gln Leu Ala	Gly Val Ala Arg Ala Tyr Asp Leu		
185	190 195		
ttg gtg ttg tca gat gag gtg tat	gag cat ctt gtt ttt gat gat cag	739	
Leu Val Leu Ser Asp Glu Val Tyr	Glu His Leu Val Phe Asp Asp Gln		
200	205 210		
aag cat gtg agt gtc gcg aag ctg	ccc ggt atg tgg gat cgc acg gtg	787	
Lys His Val Ser Val Ala Lys Leu	Pro Gly Met Trp Asp Arg Thr Val		
215	220 225		
acg gtg tcg tcg gcg gcg aaa acg	ttc aat gtg act ggt tgg aag acg	835	
Thr Val Ser Ser Ala Ala Lys Thr	Phe Asn Val Thr Gly Trp Lys Thr		
230	235 240 245		
ggg tgg gcg ttg gca ccg gag ccg	ttg ttg gag gcg gtg ttg aag gcg	883	
Gly Trp Ala Leu Ala Pro Glu Pro	Leu Leu Glu Ala Val Leu Lys Ala		
250	255 260		
aag cag ttt atg tct tat gtg ggg	gct aca cct ttt cag ccg gct gtg	931	
Lys Gln Phe Met Ser Tyr Val Gly	Ala Thr Pro Phe Gln Pro Ala Val		
265	270 275		
gcg cat gcg att gaa cat gag cag	aag tgg gtg tca aag atg tct aag	979	
Ala His Ala Ile Glu His Glu Gln	Lys Trp Val Ser Lys Met Ser Lys		
280	285 290		
ggg ctt gag ctc aag cgg gat att	ttg cgt act gcg tta gat aag gcg		
1027			
Gly Leu Glu Leu Lys Arg Asp Ile	Leu Arg Thr Ala Leu Asp Lys Ala		
295	300 305		
ggg ctg aag act cat gac agt atg	ggc acg tat ttc atc gtt gcg gat		
1075			
Gly Leu Lys Thr His Asp Ser Met	Gly Thr Tyr Phe Ile Val Ala Asp		
310	315 320 325		
att ggg gat cgt gat ggt gcg gag	ttc tgt ttt gag ttg att gag aag		
1123			
Ile Gly Asp Arg Asp Gly Ala Glu	Phe Cys Phe Glu Leu Ile Glu Lys		
330	335 340		

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag  
 1171  
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys  
                   345                                  350                                  355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg  
 1219  
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr  
                   360                                  365                                  370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta  
 1261  
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu  
                   375                                  380                                  385

tagtttgaac aggttggttg ggg  
 1284

<210> 472

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Ser Asn Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr  
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Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn  
                   20                                  25                                  30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu  
                   35                                  40                                  45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly  
                   50                                  55                                  60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu  
                   65                                  70                                  75                                  80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val  
                   85                                  90                                  95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro  
                   100                                  105                                  110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala  
                   115                                  120                                  125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu  
                   130                                  135                                  140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val  
                   145                                  150                                  155                                  160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr  
                   165                                  170                                  175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala  
                   180                                  185                                  190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu  
 195 200 205  
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met  
 210 215 220  
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val  
 225 230 235 240  
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu  
 245 250 255  
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro  
 260 265 270  
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val  
 275 280 285  
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr  
 290 295 300  
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr  
 305 310 315 320  
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe  
 325 330 335  
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe  
 340 345 350  
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys  
 355 360 365  
 Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile  
 370 375 380  
 Lys Lys Leu  
 385

<210> 473  
 <211> 607  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(607)  
 <223> FRXA00116

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 Met Thr Gln Arg Ala  
 1 5  
 gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163  
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp  
 10 15 20

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ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
      25                      30                      35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
      40                      45                      50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
      55                      60                      65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
      70                      75                      80                      85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
      90                      95                      100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
      105                      110                      115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499
Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
      120                      125                      130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
      135                      140                      145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
      150                      155                      160                      165

aag cag ttg gcg
Lys Gln Leu Ala 607

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&lt;210&gt; 474

&lt;211&gt; 169

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 474

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Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
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Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
      35                      40                      45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
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Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
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											ttg	ctg	cgc	gat	tct		
											Leu	Leu	Arg	Asp	Ser		
											1				5		
caa cga gtt ggc ctc gcc atc gat cct tcg atc gct ttg gtg atg gcc																163	
Gln	Arg	Val	Gly	Leu	Ala	Ile	Asp	Pro	Ser	Ile	Ala	Leu	Val	Met	Ala		
				10					15					20			
act tct ggt tct aca ggt acc ccg aag ggc gct cag ctc act ccg ttg																211	
Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	Gln	Leu	Thr	Pro	Leu		
			25					30					35				
aat ttg gtg agt tcc gcc gat gct acg cat cag ttt tta ggt ggc gaa																259	
Asn	Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	Phe	Leu	Gly	Gly	Glu		
		40					45					50					
ggc cag tgg ttg ctt gcc atg cca gca cac cac att gca ggc atg cag																307	
Gly	Gln	Trp	Leu	Leu	Ala	Met	Pro	Ala	His	His	Ile	Ala	Gly	Met	Gln		
		55				60					65						
gtg ctt ctt cga agc ctc att gct gga gtt gag cca cta gct att gat																355	
Val	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	Pro	Leu	Ala	Ile	Asp		
	70				75					80					85		
ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa																403	
Leu	Ser	Thr	Gly	Phe	His	Ile	Asp	Ala	Phe	Ala	Gly	Ala	Ala	Ala	Glu		
				90					95					100			

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451  
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln  
                   105                                  110                                  115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499  
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu  
                   120                                  125                                  130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547  
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg  
                   135                                  140                                  145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595  
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser  
                   150                                  155                                  160                                  165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643  
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly  
                                   170                                  175                                  180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691  
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met  
                                   185                                  190                                  195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739  
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn  
                   200                                  205                                  210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787  
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile  
                   215                                  220                                  225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840  
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His  
                   230                                  235                                  240

tgc 843

&lt;210&gt; 476

&lt;211&gt; 240

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 476

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile  
   1                                  5                                  10                                  15

Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala  
                   20                                  25                                  30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln  
                   35                                  40                                  45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His  
                   50                                  55                                  60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu  
                   65                                  70                                  75                                  80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

85										90					95				
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser				
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Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile				
		115					120					125							
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu				
		130				135					140								
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val				
145					150					155					160				
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly				
			165						170					175					
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu				
			180					185					190						
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His				
		195					200					205							
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu				
	210					215					220								
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His				
225					230					235					240				

&lt;210&gt; 477

&lt;211&gt; 1017

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(994)

&lt;223&gt; RXS00393

&lt;400&gt; 477

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ccc	cag	ccg	aat	tct	gta	act	ttg	tcc	gat	tgg	att	caa	ggc	gca	cgc	163
Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp	Ile	Gln	Gly	Ala	Arg	
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ccg	cgt	acc	tgg	gca	aat	gcg	ttc	gcg	cct	gtc	att	gcc	ggg	tca	ggg	211
Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val	Ile	Ala	Gly	Ser	Gly	
			25				30						35			

gtc	gcc	gct	ttt	cat	gat	ggg	ttt	gtg	tgg	tgg	aag	gcc	ttg	ctg	gcg	259
Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala	
		40					45					50				



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Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
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tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
120 125 130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc	643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
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Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	

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 Ala Leu Ala Phe Ser  
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 <211> 298  
 <212> PRT  
 <213> Corynebacterium glutamicum

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                   20                  25                  30  
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp  
           35                  40                  45  
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
   50                  55                  60  
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp  
   65                  70                  75                  80  
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
                   85                  90                  95  
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
           100                  105                  110  
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
           115                  120                  125  
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
   130                  135                  140  
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
   145                  150                  155                  160  
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser  
           165                  170                  175  
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
           180                  185                  190  
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
           195                  200                  205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
   210                  215                  220  
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
   225                  230                  235                  240  
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
           245                  250                  255  
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp

260 265 270

Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala  
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Val Leu Thr Gly Leu Ala Leu Ala Phe Ser  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(982)  
 <223> FRXA00393

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 Met Ser His Thr Glu  
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ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163  
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ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211  
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly  
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 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala  
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tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355  
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu  
 70 75 80 85

cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403  
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala  
 90 95 100

gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451  
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser  
 105 110 115

ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499  
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu  
 120 125 130

ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547  
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly  
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595  
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met  
 150 155 160 165  
 gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643  
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala  
 170 175 180  
 gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691  
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn  
 185 190 195  
 aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739  
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu  
 200 205 210  
 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787  
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu  
 215 220 225  
 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835  
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp  
 230 235 240 245  
 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883  
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala  
 250 255 260  
 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931  
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser  
 265 270 275  
 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979  
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 280 285 290

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 1005  
 His

<210> 480  
 <211> 294  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp  
 35 40 45  
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val  
 50 55 60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Il Arg Gly Thr Asp Glu Asp  
 65 70 75 80  
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys  
 85 90 95  
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala  
 100 105 110  
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly  
 115 120 125  
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro  
 130 135 140  
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly  
 145 150 155 160  
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser  
 165 170 175  
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly  
 180 185 190  
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr  
 195 200 205  
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys  
 210 215 220  
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu  
 225 230 235 240  
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu  
 245 250 255  
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp  
 260 265 270  
 Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro  
 275 280 285  
 Cys Ser Arg Ala Trp His  
 290

&lt;210&gt; 481

&lt;211&gt; 987

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(964)

&lt;223&gt; RXS00446

&lt;400&gt; 481

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 Met Gly Ala Val Glu

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ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	gtt	gag	ttt	gac	cag	gtc	163	
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val		
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acg	gta	ggc	tgc	ggc	tcg	tct	gcg	ctg	tgt	caa	cag	ctg	gtt	cag	gca	211	
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala		
				25					30					35			
acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259	
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu		
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gct	tat	cca	att	ttc	gcg	cag	gtc	gcg	ggc	gcc	act	cct	gtt	gcc	att	307	
Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile		
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ccg	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355	
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala		
				70					75					80			
atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403	
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro		
				90					95					100			
tcg	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451	
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys		
				105					110					115			
gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499	
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe		
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aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547	
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His		
				135					140					145			
gac	aac	gtg	att	ggc	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595	
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala		
				150					155					160			
ggc	ttg	cgt	gtt	ggc	tac	gcc	ttc	gga	aac	gca	gag	atc	atc	gca	gcg	643	
Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala		
				170					175					180			
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg	691	
Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala		
				185					190					195			
gca	gcg	ctt	gcg	agt	ttg	aat	tct	gcc	gat	gag	ttg	atg	gaa	cgg	gtg	739	
Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val		
				200					205					210			
gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggc	gct	787	
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala		
				215					220					225			
gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct	835	
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala		
				230					235					240			
														245			

tgc 987

<213> Corynebacterium glutamicum

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu  
195 200 205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val  
 210 215 220  
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro  
 225 230 235 240  
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile  
 245 250 255  
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala  
 260 265 270  
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 275 280 285

<210> 483  
 <211> 545  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1) .. (522)  
 <223> FRXA00446

<400> 483  
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 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
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 ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96  
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Ile  
 20 25 30  
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45  
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60  
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125



ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140  
 cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160  
 act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522  
 Thr Asp Lys Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170  
 tagtctttgg cgttttgcgg tgc 545

<210> 484  
 <211> 174  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 484  
 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr  
 1 5 10 15  
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile  
 20 25 30  
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr  
 35 40 45  
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile  
 50 55 60  
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala  
 65 70 75 80  
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met  
 85 90 95  
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala  
 100 105 110  
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu  
 115 120 125  
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile  
 130 135 140  
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu  
 145 150 155 160  
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly  
 165 170

<210> 485  
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 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) .. (1207)

&lt;223&gt; RXS00618

&lt;400&gt; 485

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gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
                                         Met Gln Met Leu Asp
                                         1           5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                        10                15                20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                        25                30                35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                        40                45                50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55                60                65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                        70                75                80                85

ggt gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr
                        90                95                100

gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
                        105                110                115

tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
                        120                125                130

ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
                        135                140                145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
150                155                160                165

ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
                        170                175                180

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
                        185                190                195

ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739

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Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr  
 200 205 210  
 ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787  
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile  
 215 220 225  
 gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835  
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu  
 230 235 240 245  
 tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883  
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe  
 250 255 260  
 act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931  
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg  
 265 270 275  
 gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979  
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly  
 280 285 290  
 act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct  
 1027  
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser  
 295 300 305  
 gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa  
 1075  
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu  
 310 315 320 325  
 gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc  
 1123  
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly  
 330 335 340  
 cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att  
 1171  
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile  
 345 350 355  
 gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac  
 1217  
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 360 365  
 taggttagtt tcg  
 1230

&lt;210&gt; 486

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp  
 1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
 20 25 30  
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr  
 35 40 45  
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp  
 50 55 60  
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val  
 65 70 75 80  
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu  
 85 90 95  
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr  
 100 105 110  
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys  
 115 120 125  
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu  
 130 135 140  
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr  
 145 150 155 160  
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys  
 165 170 175  
 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met  
 180 185 190  
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala  
 195 200 205  
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg  
 210 215 220  
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn  
 225 230 235 240  
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala  
 245 250 255  
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His  
 260 265 270  
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro  
 275 280 285  
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu  
 290 295 300  
 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu  
 305 310 315 320  
 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe  
 325 330 335  
 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser

340	345	350
Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys		
355	360	365
Lys		
<210> 487		
<211> 657		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
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<222> (101)..(634)		
<223> FRXA00618		
<400> 487		
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caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115		
		Met Ser Phe Gly Arg
		1 5
ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163		
Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly		
	10	15 20
acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211		
Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile		
	25	30 35
atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259		
Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser		
	40	45 50
ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307		
Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala		
	55	60 65
ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355		
Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr		
	70	75 80 85
cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403		
Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu		
	90	95 100
ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451		
Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val		
	105	110 115
tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499		
Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp		
	120	125 130
gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547		
Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu		
	135	140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595  
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr  
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644  
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys  
 170 175

taggttagtt tcg 657

<210> 488

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn  
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp  
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu  
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala  
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala  
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu  
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr  
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala  
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp  
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala  
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile  
 165 170 175

Lys Lys

<210> 489

<211> 385

<212> DNA

<213> Corynebacterium glutamicum

<220>

&lt;221&gt; CDS

&lt;222&gt; (101)..(385)

&lt;223&gt; FRXA00627

&lt;400&gt; 489

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gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115  
 Met Gln Met Leu Asp  
 1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163  
 Arg Val His Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys  
 10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211  
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala  
 25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259  
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly  
 40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307  
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr  
 55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355  
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser  
 70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385  
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 90 95

&lt;210&gt; 490

&lt;211&gt; 95

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 490

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp  
 1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala  
 20 25 30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr  
 35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp  
 50 55 60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val  
 65 70 75 80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr  
 85 90 95

<210> 491  
 <211> 1221  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(1198)  
 <223> RXS01105

<400> 491  
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 gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115  
 Met Thr Lys Ile Thr  
 1 5  
 ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163  
 Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr  
 10 15 20  
 ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211  
 Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn  
 25 30 35  
 cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259  
 Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val  
 40 45 50  
 gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307  
 Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val  
 55 60 65  
 gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355  
 Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val  
 70 75 80 85  
 gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403  
 Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile  
 90 95 100  
 ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451  
 Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu  
 105 110 115  
 gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499  
 Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr  
 120 125 130  
 cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547  
 His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp  
 135 140 145  
 atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595  
 Met Asp Val Ala Leu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val  
 150 155 160 165  
 ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643  
 Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp  
 170 175 180



gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691  
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp  
185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739  
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu  
200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787  
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala  
215 220 225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835  
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala  
230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883  
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala  
250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931  
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr  
265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979  
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala  
280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt  
1027  
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe  
295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt  
1075  
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe  
310 315 320 325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg  
1123  
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu  
330 335 340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca  
1171  
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala  
345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca  
1218  
Ala Ala Glu Ile Ile Lys Leu Asn Leu  
360 365

tga  
1221

&lt;210&gt; 492

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 492

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Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg
 1           5           10           15

Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
           20           25           30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
           35           40           45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
           50           55           60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
           65           70           75           80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
           85           90           95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
           100          105          110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
           115          120          125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
           130          135          140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
           145          150          155          160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
           165          170          175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
           180          185          190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
           195          200          205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
           210          215          220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
           225          230          235          240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
           245          250          255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
           260          265          270

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
           275          280          285

Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
           290          295          300

Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
           305          310          315          320

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Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly  
325 330 335

Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp  
340 345 350

Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu  
355 360 365

<210> 493

**<211> 1752**

**<212> DNA**

<213> Corynebacterium glutamicum

**<220>**

**<221> CDS**

<222> (101) .. (1729)

<223> RXS02315

<400> 493

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gaatcgtatc cgtacctgga gacgatctag actgttggtgc atg tcc agc acg cca 115  
Met Ser Ser Thr Pro  
1 5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163  
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val  
10 15 20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211  
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu  
25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259  
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu  
40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307  
Arg Ser Ala .Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg  
55 60 65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355  
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu  
70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403  
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu  
90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451  
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr  
105 110 115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499  
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile  
120 125 130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547

Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly		
135						140					145						
gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg 595																	
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu		
150					155					160					165		
gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643																	
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser		
				170					175					180			
tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691																	
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly		
			185					190					195				
gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739																	
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
		200					205					210					
ctg gaa gat gtg ccc acc atc gct gaa cct act gca cca aag cct tat 787																	
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
		215				220					225						
aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc 835																	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
230					235					240					245		
tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg 883																	
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
				250					255					260			
gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat 931																	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
			265					270					275				
cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat 979																	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
		280					285					290					
ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc																	
1027																	
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
		295				300					305						
acc cag gaa aag cag tgg cta aag atc tgt tcg gca gca tca gaa ctt																	
1075																	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		
310					315					320					325		
gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc																	
1123																	
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe		
				330					335					340			
acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc																	
1171																	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly		
			345					350					355				
gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg																	
1219																	

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu  
 360 365 370  
 gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc  
 1267  
 Val Gly M t Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val  
 375 380 385  
 gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct  
 1315  
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala  
 390 395 400 405  
 gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc  
 1363  
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala  
 410 415 420  
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc  
 1411  
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile  
 425 430 435  
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac  
 1459  
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn  
 440 445 450  
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt  
 1507  
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly  
 455 460 465  
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc  
 1555  
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser  
 470 475 480 485  
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac  
 1603  
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp  
 490 495 500  
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc  
 1651  
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser  
 505 510 515  
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca  
 1699  
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala  
 520 525 530  
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt  
 1749  
 Gln Gln Gln Ala Leu Met Asp Thr Val His  
 535 540  
 gcg  
 1752

&lt;210&gt; 494

&lt;211&gt; 543

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 494

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Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
          20          25          30

Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
          35          40          45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
          50          55          60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
          65          70          75          80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
          85          90          95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
          100          105          110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
          115          120          125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
          130          135          140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
          145          150          155          160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
          165          170          175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
          180          185          190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
          195          200          205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
          210          215          220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
          225          230          235          240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
          245          250          255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
          260          265          270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
          275          280          285

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Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr  
 290 295 300

Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser  
 305 310 315 320

Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn  
 325 330 335

Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp  
 340 345 350

Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile  
 355 360 365

Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe  
 370 375 380

Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile  
 385 390 395 400

Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala  
 405 410 415

Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile  
 420 425 430

Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr  
 435 440 445

Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu  
 450 455 460

Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr  
 465 470 475 480

Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu  
 485 490 495

His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp  
 500 505 510

Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg  
 515 520 525

Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His  
 530 535 540

<210> 495

<211> 1434

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1411)

<223> RXS02550

<400> 495

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				Val	Thr	Thr	Asp	Lys	
				1				5	
cgc	aaa	acc	tct	aag	acc	acc	gac	acc	163
Arg	Lys	Thr	Ser	Lys	Thr	Thr	Asp	Thr	
				10				15	
gat	cag	gca	gcg	cgt	ccc	act	cgg	cga	211
Asp	Gln	Ala	Ala	Arg	Pro	Thr	Arg	Arg	
				25				30	
cag	tcg	gag	aag	atg	aag	gac	gtg	ctg	259
Gln	Ser	Glu	Lys	Met	Lys	Asp	Val	Leu	
				40				45	
gcc	gcy	gag	gcy	gaa	cgc	atg	gag	ctt	307
Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	
				55				60	
ctc	aac	acg	gga	aat	cca	gcc	gtg	ttc	355
Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	
								80	
att	atg	cgt	gac	atg	atc	gcc	aac	ctt	403
Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	
								90	
acc	tcc	aaa	ggc	att	att	ccg	gcc	cgg	451
Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	
								110	
gaa	gtt	gtg	ccc	gga	ttc	ccc	cac	ttc	499
Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	
								125	
ggc	aac	ggt	gtc	tca	gaa	cta	atc	acc	547
Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	
								140	
aac	gac	ggc	gat	gaa	gtt	ctt	atc	ccc	595
Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	
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act	gcc	gca	acc	tcc	ctg	gct	ggt	ggt	643
Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	
								170	
gat	gag	gaa	gat	gac	tgg	aac	cca	tcc	691
Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	
								185	
atc	tca	gag	aaa	acc	aaa	gct	att	gtg	739
Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	
								200	
acg	gga	gct	gtc	tac	ccg	cgc	cgg	gtg	787
Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	
								215	



gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835  
 Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg  
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883  
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro  
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931  
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val  
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979  
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr  
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc  
 1027  
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu  
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga  
 1075  
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly  
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa  
 1123  
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu  
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc  
 1171  
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser  
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc  
 1219  
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro  
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc  
 1267  
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu  
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca  
 1315  
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro  
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg  
 1363  
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu  
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag  
 1411  
 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln  
 425 430 435

tagtagttgt taggattcac cac  
1434

<210> 496

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

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Lys	Ala	Val	Gly	Ala	Asp	Gln	Ala	Ala	Arg	Pro	Thr	Arg	Arg	Thr	Thr
			20					25					30		
Arg	Arg	Ile	Phe	Asp	Gln	Ser	Glu	Lys	Met	Lys	Asp	Val	Leu	Tyr	Glu
		35					40					45			
Ile	Arg	Gly	Pro	Val	Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	Asp	Gly
	50					55					60				
His	Asn	Ile	Leu	Lys	Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	Gly	Phe
65					70					75					80
Asp	Ala	Pro	Asp	Val	Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	Pro	Thr
			85						90					95	
Ser	Gln	Gly	Tyr	Ser	Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	Arg	Ala
			100					105					110		
Val	Val	Thr	Arg	Tyr	Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	Asp	Val
		115					120					125			
Asp	Asp	Val	Phe	Leu	Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	Met	Thr
	130					135					140				
Thr	Gln	Ala	Leu	Leu	Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	Ala	Pro
145					150					155					160
Asp	Tyr	Pro	Leu	Trp	Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	Lys	Pro
			165						170					175	
Val	His	Tyr	Leu	Cys	Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	Ile	Glu
			180					185					190		
Asp	Ile	Lys	Ser	Lys	Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	Ile
		195					200					205			
Asn	Pro	Asn	Asn	Pro	Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	Leu	Glu
	210					215					220				
Gln	Ile	Val	Glu	Ile	Ala	Arg	Glu	His	Asp	Leu	Leu	Ile	Leu	Ala	Asp
225					230					235					240
Glu	Ile	Tyr	Asp	Arg	Ile	Leu	Tyr	Asp	Asp	Ala	Glu	His	Ile	Ser	Leu
			245						250					255	
Ala	Thr	Leu	Ala	Pro	Asp	Leu	Leu	Cys	Ile	Thr	Tyr	Asn	Gly	Leu	Ser
		260						265					270		

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr  
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 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu  
           290                                  295                                  300  
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln  
 305                                  310                                  315                                  320  
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His  
                                   325                                  330                                  335  
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu  
                                   340                                  345                                  350  
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe  
                                   355                                  360                                  365  
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu  
           370                                  375                                  380  
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr  
 385                                  390                                  395                                  400  
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro  
                                   405                                  410                                  415  
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu  
                                   420                                  425                                  430  
 Ser Thr Tyr Lys Gln  
           435

&lt;210&gt; 497

&lt;211&gt; 1080

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1057)

&lt;223&gt; RXS02319

&lt;400&gt; 497

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agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115  
   Met Ser Asn Tyr Ser  
   1                                  5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163  
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe  
                                   10                                  15                                  20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211  
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg  
                                   25                                  30                                  35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259  
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn

40	45	50	
gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65			307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85			355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100			403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 105 110 115			451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130			499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145			547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165			595
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 170 175 180			643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195			691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210			739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225			787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245			835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260			883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275			931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290			979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa  
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu  
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct  
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1080

<210> 498

<211> 319

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 498

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Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg  
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr  
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu  
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys  
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala  
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp  
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val  
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn  
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu  
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp  
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met  
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

210	215	220	
Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp			
225	230	235	240
His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn			
	245	250	255
Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu			
	260	265	270
Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr			
	275	280	285
Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe			
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Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr			
305	310	315	
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		Leu Lys Leu His Pro	5
		1	
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg			163
Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala			
	10	15	20
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc			211
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala			
	25	30	35
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac			259
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp			
	40	45	50
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct			307
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser			
	55	60	65
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag			355
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys			
	70	75	80
			85
ctg ttt tagtcttcat tcttgctggc tgc			384
Leu Phe			

&lt;210&gt; 500

&lt;211&gt; 87

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 500

Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys  
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Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly  
 20 25 30

Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val  
 35 40 45

Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu  
 50 55 60

Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg  
 65 70 75 80

Arg Ala Ile Ala Lys Leu Phe  
 85

&lt;210&gt; 501

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(775)

&lt;223&gt; RXS03003

&lt;400&gt; 501

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caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115  
 Met Thr Ser Arg Thr  
 1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163  
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser  
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gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211  
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser  
 25 30 35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259  
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu  
 40 45 50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307  
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro  
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gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355

Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met  
 70 75 80 85  
 aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403  
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu  
 90 95 100  
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451  
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val  
 105 110 115  
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499  
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala  
 120 125 130  
 gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547  
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln  
 135 140 145  
 atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595  
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys  
 150 155 160 165  
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643  
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu  
 170 175 180  
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691  
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp  
 185 190 195  
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739  
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp  
 200 205 210  
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 215 220 225  
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 <212> PRT  
 <213> Corynebacterium glutamicum  
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 20 25 30  
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 35 40 45  
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln  
 50 55 60  
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu  
 65 70 75 80



Arg	Arg	Tyr	Asn	Met	Thr	Lys	Leu	Val	Asp	Ala	Ser	Leu	Leu	Pro	Val	
				85					90					95		
Val	Gly	Thr	Lys	Glu	Ala	Ile	Ala	Leu	Leu	Pro	Phe	Ala	Leu	Gly	Ile	
				100					105					110		
Ser	Gly	Thr	Val	Val	Ile	Pro	Glu	Ile	Ala	Tyr	Pro	Thr	Tyr	Glu	Val	
				115					120					125		
Ala	Val	Val	Ala	Ala	Gly	Cys	Thr	Val	Leu	Arg	Ser	Asp	Ser	Leu	Phe	
				130					135					140		
Lys	Leu	Gly	Pro	Gln	Ile	Pro	Ser	Met	Met	Phe	Ile	Asn	Ser	Pro	Ser	
				145					150					155		
Asn	Pro	Thr	Gly	Lys	Val	Leu	Gly	Ile	Pro	His	Leu	Arg	Lys	Val	Val	
				165					170					175		
Lys	Trp	Ala	Gln	Glu	Asn	Asn	Val	Ile	Leu	Ala	Ala	Asp	Glu	Cys	Tyr	
				180					185					190		
Leu	Gly	Leu	Gly	Trp	Asp	Asp	Glu	Asn	Pro	Pro	Ile	Ser	Ile	Leu	Asp	
				195					200					205		
Pro	Arg	Val	Cys	Asp	Gly	Asp	His	Thr	Asn	Leu	Ile	Ala	Ile	His	Ser	
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Leu																
225																

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Met Pro Gly Lys Ile  
1 5

ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163  
Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro  
10 15 20

gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211  
Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr  
25 30 35

gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259  
Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn  
40 45 50

cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307

His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His  
 55 60 65  
 atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355  
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg  
 70 75 80 85  
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 Phe Trp Met Leu

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 <212> PRT  
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 Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu  
 35 40 45  
 Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn  
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 Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr  
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 Met Thr Gln Ser Ala  
 1 5  
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163  
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn  
 10 15 20  
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211  
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu  
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259  
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu  
           40                                  45                                  50  
  
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307  
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile  
           55                                  60                                  65  
  
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355  
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala  
           70                                  75                                  80                                  85  
  
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403  
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala  
                                   90                                  95                                  100  
  
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451  
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala  
                                   105                                  110                                  115  
  
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499  
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           120                                  125                                  130  
  
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 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr  
           135                                  140                                  145  
  
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595  
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys  
           150                                  155                                  160                                  165  
  
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 Gln

&lt;210&gt; 506

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 506

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 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu  
           20                                  25                                  30  
  
 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe  
           35                                  40                                  45  
  
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly  
           50                                  55                                  60  
  
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val  
           65                                  70                                  75                                  80  
  
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val  
                                   85                                  90                                  95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr  
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr  
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe  
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Glu Ala Pro Ile Lys Gln  
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 Val Leu Gly Ala Val  
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163  
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp  
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gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211  
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val  
 25 30 35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259  
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu  
 40 45 50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307  
 Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met  
 55 60 65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc 355  
 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly  
 70 75 80 85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403  
 Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys  
 90 95 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451  
 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val  
 105 110 115

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Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
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Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
135 140 145	
ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc	595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
150 155 160 165	
gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag	643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
170 175 180	
caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc	691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
185 190 195	
cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat	739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
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Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt	883
Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu	
250 255 260	
cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg	931
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val	
265 270 275	
ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac	979
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr	
280 285 290	
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc	
1027	
Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser	
295 300 305	
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Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu	
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330 335 340	

gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg  
 1171  
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu  
 345 350 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac  
 1219  
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 360 365 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc  
 1267  
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg  
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg  
 1315  
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu  
 390 395 400 405

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 1363  
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu  
 410 415 420

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 1411  
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu  
 425 430 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc  
 1459  
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe  
 440 445 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc  
 1507  
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val  
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt  
 1555  
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe  
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag  
 1603  
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu  
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc  
 1651  
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr  
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cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg  
 1699  
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu  
 520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat  
 1747  
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp  
 535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc  
 1795  
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala  
 550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc  
 1843  
 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala  
 570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag  
 1891  
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu  
 585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta  
 1939  
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val  
 600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg  
 1987  
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val  
 615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt  
 2035  
 Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly  
 630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc  
 2083  
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr  
 650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag  
 2131  
 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys  
 665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg  
 2179  
 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro  
 680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc  
 2227  
 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala  
 695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc  
 2275  
 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val  
 710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc  
2323  
Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro  
730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc  
2371  
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr  
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct  
2419  
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro  
760 765 770

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2467  
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met  
775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc  
2515  
Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala  
790 795 800 805

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Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln  
810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct  
2611  
Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro  
825 830 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat  
2659  
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp  
840 845 850

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2707  
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser  
855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc  
2755  
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser  
870 875 880 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc  
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Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser  
890 895 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc  
2851  
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala  
905 910 915



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 2899  
 Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr  
           920                          925                          930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg  
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 Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro  
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 2995  
 Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser  
           950                          955                          960                          965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt  
 3043  
 Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu  
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 Val Gly Trp

<210> 508

<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

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Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu  
           20                          25                          30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile  
           35                          40                          45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln  
           50                          55                          60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln  
           65                          70                          75                          80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr  
                           85                          90                          95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val  
           100                          105                          110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu  
           115                          120                          125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu  
           130                          135                          140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile  
           145                          150                          155                          160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile  
 165 170 175  
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val  
 180 185 190  
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala  
 195 200 205  
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met  
 210 215 220  
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala  
 225 230 235 240  
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala  
 245 250 255  
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu  
 260 265 270  
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn  
 275 280 285  
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu  
 290 295 300  
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu  
 305 310 315 320  
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr  
 325 330 335  
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser  
 340 345 350  
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu  
 355 360 365  
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly  
 370 375 380  
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu  
 385 390 395 400  
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala  
 405 410 415  
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe  
 420 425 430  
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val  
 435 440 445  
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser  
 450 455 460  
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro  
 465 470 475 480

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val  
 485 490 495  
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser  
 500 505 510  
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val  
 515 520 525  
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe  
 530 535 540  
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln  
 545 550 555 560  
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp  
 565 570 575  
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala  
 580 585 590  
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu  
 595 600 605  
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn  
 610 615 620  
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala  
 625 630 635 640  
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala  
 645 650 655  
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala  
 660 665 670  
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala  
 675 680 685  
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp  
 690 695 700  
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu  
 705 710 715 720  
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala  
 725 730 735  
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr  
 740 745 750  
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu  
 755 760 765  
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr  
 770 775 780  
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val  
 785 790 795 800  
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser

805								810				815				
Ser	Thr	Asn	Glu	Gln	Ser	Pro	Leu	Ala	Ser	Val	Glu	Ala	Thr	Thr	Ser	
820								825				830				
Ala	Thr	Pro	Glu	Pro	Val	Gly	Pro	Pro	Val	Tyr	Leu	Asp	Leu	Asp	Gln	
835								840				845				
Ala	Arg	Thr	Trp	Asp	Asp	Gly	Ala	Gly	Thr	Asp	Val	Thr	Asp	Val	Thr	
850								855				860				
Asp	Gly	Asn	Thr	Ser	Thr	Ala	Trp	Thr	Ser	Thr	Gly	Gly	Asp	Gly	Leu	
865								870				875				
Leu	Val	Asp	Leu	Ser	Thr	Pro	Ala	Arg	Leu	Asp	Arg	Val	Ile	Leu	Thr	
885								890				895				
Thr	Gly	Thr	Gly	Ser	Asp	Ser	Asn	Val	Thr	Ser	Thr	Val	Lys	Ile	Tyr	
900								905				910				
Ala	Phe	Asn	Asp	Ala	Ser	Pro	His	Ser	Leu	Ser	Glu	Gly	Ile	Glu	Ile	
915								920				925				
Gly	Thr	Val	Asp	Tyr	Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp	
930								935				940				
Ser	Ser	Lys	Leu	Pro	Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp	
945								950				955				
Glu	Val	Arg	Ser	Ser	Gln	Thr	Ser	Asp	Thr	Asn	Pro	Gln	Met	Gln	Ile	
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 <213> *Corynebacterium glutamicum*

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 <223> RXC02080

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 Met Ser Ile Glu Trp  
 1 5  
 tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca 163  
 Leu Gln Ile Val 10 Leu Gly Ala Ile 15 Phe Gly Ala Gly Phe Leu Ala 20  
 gga agc atc aat gta att gtc gga gca gga aca tta gtg tcg ttt cct 211  
 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro  
 25 30 35

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac	259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn	
40 45 50	
acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga	307
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
55 60 65	
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca	355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
90 95 100	
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg	451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
120 125 130	
act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc	547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
135 140 145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg	595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
150 155 160 165	
tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg	643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
170 175 180	
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa	691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
185 190 195	
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata	739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
200 205 210	
atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg	787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala	
215 220 225	
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga	835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
230 235 240 245	
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
250 255 260	
acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc	930
Thr Val Ile Val Met Thr Ile Gly	
265	

&lt;210&gt; 510

&lt;211&gt; 269

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 510

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Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr  
 20 25 30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr  
 35 40 45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly  
 50 55 60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg  
 65 70 75 80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu  
 85 90 95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu  
 100 105 110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys  
 115 120 125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln  
 130 135 140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala  
 145 150 155 160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile  
 165 170 175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu  
 180 185 190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala  
 195 200 205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr  
 210 215 220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly  
 225 230 235 240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val  
 245 250 255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly  
 260 265

&lt;210&gt; 511

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(646)

&lt;223&gt; RXC02789

&lt;400&gt; 511

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                                         Met Lys Val Ser Ala
                                         1 5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
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gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
                        25 30 35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
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Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
                        55 60 65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga 355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
                        70 75 80 85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                        90 95 100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
                        105 110 115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
                        120 125 130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca 547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
                        135 140 145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
                        150 155 160 165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
                        170 175 180

gga tgaaccaa at ccgaaaccgc cgg 669
Gly

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<210> 512  
 <211> 182  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 512

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Arg Arg Leu Gly Leu Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala
 20             25             30

Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg
 35             40             45

Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val
 50             55             60

Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro
 65             70             75             80

Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu
 85             90             95

Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile
 100            105            110

Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln
 115            120            125

Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile
 130            135            140

Asp Gln Ala Ala Ala Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg
 145            150            155            160

Thr Arg Ala Leu Glu Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu
 165            170            175

Lys Gly Asn Phe Pro Gly
 180

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<210> 513  
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<220>  
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 <222> (101)..(880)  
 <223> RXC02295

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gatgcaagac tgataccggg atgtgatagg agcgcaccac atg ggg ttg gaa tta 115
Met Gly Leu Glu Leu
 1             5

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gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly	163
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25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	259
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	307
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	355
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	403
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	451
105 110 115	
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	499
120 125 130	
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	547
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	595
150 155 160 165	
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	643
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	691
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	739
200 205 210	
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	787
215 220 225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	835
230 235 240 245	

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880  
Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met  
250 255 260

tagataagtc ggggcaaact cta 903

**<210> 514**

**<211> 260**

<212> PRT

<213> Corynebacterium glutamicum

**<400> 514**

Met Gly Leu Glu Leu Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly  
1 5 10 15

Ala Ala Val Ala Gly Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu  
20 25 30

Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val  
35 40 45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser  
50 55 60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu  
65 70 75 80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu  
85 90 95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val  
100 105 110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly  
115 120 125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala  
130 135 140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro  
145 150 155 160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln  
165 170 175

Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr  
180 185 190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp  
195 200 205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu  
210 215 220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala  
225 230 235 240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln  
245 250 255

Ile Gln Gly Met  
260

<210> 515  
<211> 1132  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (101) .. (1132)  
<223> RXN03063

<400> 515  
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acctagacaa cagtttgtat ctcacctcac aggaggaacc gtg gaa gat ctc tca 115  
Val Glu Asp Leu Ser  
1 5

tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg 163  
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro  
10 15 20

aag tcg aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca 211  
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala  
25 30 35

ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc 259  
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile  
40 45 50

ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307  
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile  
55 60 65

gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355  
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val  
70 75 80 85

ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403  
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro  
90 95 100

tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451  
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro  
105 110 115

ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499  
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala  
120 125 130

gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547  
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala  
135 140 145

gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595  
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met  
150 155 160 165

gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta 643  
 Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu  
 170 175 180

gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691  
 Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly  
 185 190 195

ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739  
 Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile Ser Val Ile Glu Ser  
 200 205 210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787  
 Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln  
 215 220 225

ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835  
 Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly Phe Leu Ala Ala Ile  
 230 235 240 245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883  
 Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile  
 250 255 260

caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931  
 Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu  
 265 270 275

ggt gtg atc ccc gac gtc atc acc acc gca aaa ggc atc gcc ggc ggc 979  
 Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly  
 280 285 290

atg cca cta tcc gca gtg acc ggc cgc gca gaa atc atg gac gca ccc  
 1027  
 Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu Ile Met Asp Ala Pro  
 295 300 305

ggc ccc ggc gcg ctc ggc gga acc tac ggc gga aac ccc gtt gct tgc  
 1075  
 Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly Asn Pro Val Ala Cys  
 310 315 320 325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag  
 1123  
 Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu Gln Ala Asp Leu Lys  
 330 335 340

acc cgc gcg  
 1132  
 Thr Arg Ala

&lt;210&gt; 516

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 516

Val Glu Asp Leu Ser Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu  
 1 5 10 15

Gln Val Pro Gly Pro Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala  
                   20                  25                  30  
 Ala Val Ala Arg Ala Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp  
                   35                  40                  45  
 Ala Asp Gly Gly Ile Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp  
                   50                  55                  60  
 Leu Ala Ser Gly Ile Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala  
                   65                  70                  75                  80  
 Val Ala Lys Ala Val Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys  
                   85                  90                  95  
 Phe Met Val Ser Pro Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu  
                   100                  105                  110  
 Asn Ala Leu Thr Pro Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn  
                   115                  120                  125  
 Ser Gly Ala Glu Ala Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr  
                   130                  135                  140  
 Thr Gly Lys Gly Ala Val Val Val Phe Asp Asn Ala Tyr His Gly Arg  
                   145                  150                  155                  160  
 Thr Asn Leu Thr Met Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser  
                   165                  170                  175  
 Gly Phe Gly Pro Leu Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr  
                   180                  185                  190  
 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile  
                   195                  200                  205  
 Ser Val Ile Glu Ser Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val  
                   210                  215                  220  
 Ile Glu Pro Ile Gln Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly  
                   225                  230                  235                  240  
 Phe Leu Ala Ala Ile Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe  
                   245                  250                  255  
 Ile Ala Asp Glu Ile Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe  
                   260                  265                  270  
 Ala Ser Asp Ala Glu Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys  
                   275                  280                  285  
 Gly Ile Ala Gly Gly Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu  
                   290                  295                  300  
 Ile Met Asp Ala Pro Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly  
                   305                  310                  315                  320  
 Asn Pro Val Ala Cys Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu  
                   325                  330                  335

Gln Ala Asp Leu Lys Thr Arg Ala  
340

<210> 517  
<211> 1491  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1468)  
<223> RXN02970

<400> 517  
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ttattttaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115  
Leu Ala Leu Lys Gly  
1 5  
  
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
10 15 20  
  
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
25 30 35  
  
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
40 45 50  
  
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
55 60 65  
  
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355  
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
70 75 80 85  
  
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
90 95 100  
  
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
105 110 115  
  
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
120 125 130  
  
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
135 140 145  
  
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595  
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	
1027	
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	
1075	
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	
1123	
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	
1171	
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	
1219	
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	
1267	
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa  
1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu  
390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac  
1363

Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His  
410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg  
1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu  
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg  
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly  
440 445 450

gcg ttg ttc taagttttct agataacaag gcc  
1491

Ala Leu Phe  
455

<210> 518

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe  
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr



145		150		155		160
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg	165		170		175	
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro	180		185		190	
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys	195		200		205	
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala	210		215		220	
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly	225		230		235	240
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys	245		250		255	
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe	260		265		270	
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe	275		280		285	
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala	290		295		300	
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly	305		310		315	320
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala	325		330		335	
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile	340		345		350	
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu	355		360		365	
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile	370		375		380	
Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala	385		390		395	400
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser	405		410		415	
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu	420		425		430	
Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu	435		440		445	
Leu Thr Phe Ala Gly Ala Leu Phe	450		455			

&lt;210&gt; 519

<211> 1330  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1330)  
 <223> FRXA01009

<400> 519  
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 ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115  
 Leu Ala Leu Lys Gly  
 1 5  
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163  
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala  
 10 15 20  
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211  
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe  
 25 30 35  
 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259  
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala  
 40 45 50  
 gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307  
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp  
 55 60 65  
 atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355  
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg  
 70 75 80 85  
 tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403  
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn  
 90 95 100  
 ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451  
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val  
 105 110 115  
 tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499  
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly  
 120 125 130  
 gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547  
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly  
 135 140 145  
 cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595  
 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly  
 150 155 160 165  
 tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643  
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr  
 170 175 180  
 acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser		
			185					190					195				
tca	ttc	ttt	gcc	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aag	739	
Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
		200					205					210					
cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggg	gct	ggc	atg	atc	gca	gcg	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
	215					220					225						
atc	gtc	ctg	gag	cca	gtg	gtg	gga	tca	tca	gga	atc	atc	ctg	cca	cca	835	
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
230					235					240					245		
gca	ggg	tac	tta	aat	ggc	gtg	cgc	gaa	ctt	tgc	aac	aag	cac	ggc	atc	883	
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
				250				255						260			
ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
			265					270					275				
ctg	ttt	gct	tac	gag	cat	gct	ggc	gac	gat	ttc	cag	cca	gac	atg	atc	979	
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile		
		280					285					290					
acc	ttc	gcc	aag	ggg	gtt	aac	gca	ggg	tac	gcc	cca	ctc	ggg	ggc	atc		
1027																	
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile		
	295					300					305						
gtg	atg	acc	caa	tca	atc	cgc	gat	acc	ttc	gga	tca	gag	gca	tac	tcc		
1075																	
Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser		
310					315					320					325		
ggc	gga	ctc	acc	tac	tcc	gga	cac	cca	ctt	gca	gta	gca	ccc	gcc	aag		
1123																	
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys		
				330				335					340				
gca	gcg	ctg	gag	att	tac	gcg	gaa	gga	gag	atc	att	cca	cgc	gta	gct		
1171																	
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala		
			345				350					355					
cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa		
1219																	
Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	Arg	Glu	Leu	Ala	Glu		
		360					365					370					
gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tgg	gca		
1267																	
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala		
	375					380					385						
gtg	gag	ttc	aat	gca	gac	gcc	act	gcc	atg	gct	gcc	ggg	gct	gca	gaa		
1315																	
Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	Ala	Gly	Ala	Ala	Glu		
390					395					400					405		

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 1330  
 Phe Lys Glu Arg Gly  
 410

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 <213> Corynebacterium glutamicum

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 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp  
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 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro  
 35 40 45  
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly  
 50 55 60  
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly  
 65 70 75 80  
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg  
 85 90 95  
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val  
 100 105 110  
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe  
 115 120 125  
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala  
 130 135 140  
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr  
 145 150 155 160  
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg  
 165 170 175  
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro  
 180 185 190  
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys  
 195 200 205  
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala  
 210 215 220  
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly  
 225 230 235 240  
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys  
 245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe  
 260 265 270  
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe  
 275 280 285  
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala  
 290 295 300  
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly  
 305 310 315 320  
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala  
 325 330 335  
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile  
 340 345 350  
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu  
 355 360 365  
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile  
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 <212> DNA  
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<220>  
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 <223> RXA01551

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 Leu Lys Ala Val Pro 5  
 1  
 acg ggc gcc cga gca cgg gct gag atc gcg ctg att gct gcg cga gca 163  
 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala 20  
 10 15  
 ccg ttt gaa cct gtc cgg tta gca ccg gcg aag gaa gag agg aat ggt 211  
 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly 35  
 25 30  
 gca atg acg cct acc caa aat gag atc cac ccg aaa cat agc tac tcc 259  
 Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser 50  
 40 45  
 ccc atc cgc aag gac ggt ctc gag gtc ccg gag acc gaa atc cgc ctc 307

Pro	Ile	Arg	Lys	Asp	Gly	Leu	Glu	Val	Pro	Glu	Thr	Glu	Ile	Arg	Leu		
55						60					65						
gat	gac	tcg	cca	agc	ggc	ccc	aac	gaa	ccc	ttc	cgc	atc	tac	cgc	acc	355	
Asp	Asp	Ser	Pro	Ser	Gly	Pro	Asn	Glu	Pro	Phe	Arg	Ile	Tyr	Arg	Thr		
70					75				80						85		
cgt	ggc	cca	gaa	acc	aac	ccc	aag	cag	gga	ctt	ccg	cgg	ctg	cgc	gag	403	
Arg	Gly	Pro	Glu	Thr	Asn	Pro	Lys	Gln	Gly	Leu	Pro	Arg	Leu	Arg	Glu		
				90					95						100		
tca	tgg	atc	acc	gcc	cgc	ggc	gac	gtt	gcc	acc	tat	cag	ggg	cgc	gag	451	
Ser	Trp	Ile	Thr	Ala	Arg	Gly	Asp	Val	Ala	Thr	Tyr	Gln	Gly	Arg	Glu		
			105					110					115				
cgt	ttg	ctt	atc	gac	gac	ggc	cgc	tcg	gca	atg	cgt	cga	ggg	caa	gct	499	
Arg	Leu	Leu	Ile	Asp	Asp	Gly	Arg	Ser	Ala	Met	Arg	Arg	Gly	Gln	Ala		
			120				125					130					
tcg	gct	gag	tgg	aaa	ggc	caa	aaa	cca	gct	cct	ttg	aag	gcg	cta	cct	547	
Ser	Ala	Glu	Trp	Lys	Gly	Gln	Lys	Pro	Ala	Pro	Leu	Lys	Ala	Leu	Pro		
	135					140					145						
ggc	aaa	aga	gtc	acc	caa	atg	gcc	tat	gca	cgt	gct	ggc	gtg	att	act	595	
Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	Ala	Gly	Val	Ile	Thr		
	150				155				160						165		
cgt	gaa	atg	gag	ttt	gta	gcg	ctg	cgc	gaa	cac	gtt	gat	gcg	gag	ttt	643	
Arg	Glu	Met	Glu	Phe	Val	Ala	Leu	Arg	Glu	His	Val	Asp	Ala	Glu	Phe		
				170					175					180			
gtg	cgc	tct	gag	gtg	gcg	cgc	ggg	cgg	gcc	att	att	ccc	aac	aac	gtc	691	
Val	Arg	Ser	Glu	Val	Ala	Arg	Gly	Arg	Ala	Ile	Ile	Pro	Asn	Asn	Val		
			185					190					195				
aac	cac	ccc	gaa	tct	gaa	ccg	atg	att	att	ggg	cgc	aaa	ttt	ttg	acc	739	
Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	Arg	Lys	Phe	Leu	Thr		
		200					205					210					
aaa	atc	aac	gcc	aat	att	ggc	aat	tct	gcg	gtc	acc	tct	tca	atc	gag	787	
Lys	Ile	Asn	Ala	Asn	Ile	Gly	Asn	Ser	Ala	Val	Thr	Ser	Ser	Ile	Glu		
	215					220					225						
gaa	gag	gtg	tcc	aag	ctg	cag	tgg	gcc	acg	cgc	tgg	ggg	gcc	gat	acc	835	
Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala	Thr	Arg	Trp	Gly	Ala	Asp	Thr		
	230				235				240					245			
gtg	atg	gat	cta	tcc	acc	ggc	gat	gat	att	cac	acc	acc	cgc	gaa	tgg	883	
Val	Met	Asp	Leu	Ser	Thr	Gly	Asp	Asp	Ile	His	Thr	Thr	Arg	Glu	Trp		
				250					255					260			
att	atc	cgc	aac	tcc	ccc	gtt	cct	atc	ggc	acc	gtc	ccg	atc	tac	caa	931	
Ile	Ile	Arg	Asn	Ser	Pro	Val	Pro	Ile	Gly	Thr	Val	Pro	Ile	Tyr	Gln		
			265					270					275				
gcg	ctg	gaa	aaa	gta	aat	ggc	gtg	gcc	gca	gac	ctt	aac	tgg	gaa	gta	979	
Ala	Leu	Glu	Lys	Val	Asn	Gly	Val	Ala	Ala	Asp	Leu	Asn	Trp	Glu	Val		
	280					285						290					
ttc	cgc	gat	acc	atc	att	gag	cag	tgt	gaa	caa	ggc	gtg	gac	tat	atg		
1027																	

Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln Gly Val Asp Tyr Met  
 295 300 305  
 acc atc cac gcc ggc gtc ctg ctg gct tat atc cca ctg act acc cgt  
 1075  
 Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile Pro Leu Thr Thr Arg  
 310 315 320 325  
 cgt gtc acc ggc att gtc tcc cgc ggc gga tcc att atg gcc ggt tgg  
 1123  
 Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser Ile Met Ala Gly Trp  
 330 335 340  
 tgt ctg gcg cat cac cgc gaa tca ttc ctc tac gag cat ttc gac gag  
 1171  
 Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr Glu His Phe Asp Glu  
 345 350 355  
 ctg tgc gaa atc ttt gca caa tat gac gtc gca ttc tcc ctc ggt gat  
 1219  
 Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala Phe Ser Leu Gly Asp  
 360 365 370  
 ggc cta cgc ccc gga tcg ctt gcc gat gcc aac gac gcc gcg caa ttc  
 1267  
 Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn Asp Ala Ala Gln Phe  
 375 380 385  
 gcc gag ctg aaa acc att ggt gag ctc acc caa cgc gcc tgg gaa tac  
 1315  
 Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln Arg Ala Trp Glu Tyr  
 390 395 400 405  
 gat gta caa gta atg gtc gaa gga cct gga cac gtg cca cta aac atg  
 1363  
 Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met  
 410 415 420  
 atc cag gaa aac aac gag ctg gaa caa aag tgg gca gcg gac gca cct  
 1411  
 Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro  
 425 430 435  
 ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac  
 1459  
 Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp  
 440 445 450  
 cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc  
 1507  
 His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr  
 455 460 465  
 gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac  
 1555  
 Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn  
 470 475 480 485  
 cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac  
 1603  
 Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His

490 495 500  
 gca gca gat gtg gcc aag ggt cat ccc ggc gcg cgt gcc tgg gac gac  
 1651  
 Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp  
 505 510 515  
 gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg  
 1699  
 Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala  
 520 525 530  
 ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg  
 1747  
 Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu  
 535 540 545  
 ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg  
 1795  
 Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro  
 550 555 560 565  
 aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc  
 1843  
 Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly  
 570 575 580  
 gat caa atc gcg gaa ttg ggg atg cct ggg gtt ggg gat tct tct agt  
 1891  
 Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser  
 585 590 595  
 gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg  
 1939  
 Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg  
 600 605 610  
 gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc  
 1985  
 Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg Arg  
 615 620 625  
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 1998

&lt;210&gt; 522

&lt;211&gt; 625

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 522

Leu Lys Ala Val Pro Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu  
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Ile Ala Ala Arg Ala Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys  
 20 25 30

Glu Glu Arg Asn Gly Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro  
 35 40 45



Lys His Ser Tyr Ser Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu  
 50 55 60  
 Thr Glu Ile Arg Leu Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe  
 65 70 75 80  
 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu  
 85 90 95  
 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr  
 100 105 110  
 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met  
 115 120 125  
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro  
 130 135 140  
 Leu Lys Ala Leu Pro Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg  
 145 150 155 160  
 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His  
 165 170 175  
 Val Asp Ala Glu Phe Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile  
 180 185 190  
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly  
 195 200 205  
 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val  
 210 215 220  
 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg  
 225 230 235 240  
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His  
 245 250 255  
 Thr Thr Arg Glu Trp Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr  
 260 265 270  
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp  
 275 280 285  
 Leu Asn Trp Glu Val Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln  
 290 295 300  
 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile  
 305 310 315 320  
 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser  
 325 330 335  
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr  
 340 345 350  
 Glu His Phe Asp Glu Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala  
 355 360 365  
 Phe Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn

370	375	380
Asp Ala Ala Gln Phe Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln 385 390 395 400		
Arg Ala Trp Glu Tyr Asp Val Gln Val Met Val Glu Gly Pro Gly His 405 410 415		
Val Pro Leu Asn Met Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp 420 425 430		
Ala Ala Asp Ala Pro Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile 435 440 445		
Ala Pro Gly Tyr Asp His Ile Thr Ser Ala Ile Gly Ala Ala His Ile 450 455 460		
Ala Met Gly Gly Thr Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His 465 470 475 480		
Leu Gly Leu Pro Asn Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr 485 490 495		
Lys Leu Ala Ala His Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala 500 505 510		
Arg Ala Trp Asp Asp Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp 515 520 525		
Asn Asp Gln Phe Ala Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr 530 535 540		
His Asp Glu Thr Leu Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys 545 550 555 560		
Ser Met Cys Gly Pro Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile 565 570 575		
Arg Asp Met Phe Gly Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val 580 585 590		
Gly Asp Ser Ser Ser Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met 595 600 605		
Ala Glu Lys Ser Arg Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg 610 615 620		
Arg 625		

<210> 523  
 <211> 1013  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(990)  
 <223> RXA01019

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Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro	
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acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag	96
Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu	
20 25 30	
caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat	144
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His	
35 40 45	
gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg	192
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala	
50 55 60	
ggt agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag	240
Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln	
65 70 75 80	
aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt	288
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg	
85 90 95	
cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg	336
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	
100 105 110	
gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag	384
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu	
115 120 125	
tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg	432
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu	
130 135 140	
gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag	480
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu	
145 150 155 160	
ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga	528
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	
165 170 175	
aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt	576
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	
180 185 190	
cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc	624
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	
195 200 205	
gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga	672
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly	
210 215 220	
gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac	720
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn	
225 230 235 240	

caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
                   245                  250                  255

atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
                   260                  265                  270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
                   275                  280                  285

tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
                   290                  295                  300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
                   305                  310                  315                  320

ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg  
 1010  
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
                   325                  330

aat  
 1013

<210> 524  
 <211> 330  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 524  
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 Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu  
                   20                  25                  30  
 Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His  
                   35                  40                  45  
 Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala  
                   50                  55                  60  
 Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln  
                   65                  70                  75                  80  
 Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg  
                   85                  90                  95  
 Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val  
                   100                  105                  110  
 Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu  
                   115                  120                  125  
 Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu  
                   130                  135                  140

Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu  
 145 150 155 160  
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly  
 165 170 175  
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly  
 180 185 190  
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys  
 195 200 205  
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly  
 210 215 220  
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn  
 225 230 235 240  
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser  
 245 250 255  
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr  
 260 265 270  
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu  
 275 280 285  
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln  
 290 295 300  
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr  
 305 310 315 320  
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe  
 325 330

&lt;210&gt; 525

&lt;211&gt; 706

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(706)

&lt;223&gt; RXA01352

&lt;400&gt; 525

gtgcccaatg cattgggctg agattgcgcg ctgttgctgc gcgggaccgt tcgaacctgt 60

ctggttaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115  
 Val Phe Glu Asn Arg  
 1 5

ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163  
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu  
 10 15 20

gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211  
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

25	30	35	
cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca			259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala			
40	45	50	
tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg			307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val			
55	60	65	
ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga			355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly			
70	75	80	85
ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt			403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu			
90	95	100	
gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act			451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr			
105	110	115	
gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg			499
Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu Leu Ser Asp Val Leu			
120	125	130	
gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca			547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser			
135	140	145	
ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg			595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu			
150	155	160	165
tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg			643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val			
170	175	180	
cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct			691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala			
185	190	195	
ttt tct gaa tct gat			706
Phe Ser Glu Ser Asp			
200			

&lt;210&gt; 526

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 526

Val	Phe	Glu	Asn	Arg	Phe	Asp	Leu	Arg	Cys	Tyr	Val	Val	Thr	Gly	Ala
1				5					10					15	

Gly	Ser	Val	Asp	Glu	Val	Val	His	Thr	Ala	Ser	Ala	Ala	Ala	Arg	Gly
			20					25					30		

Gly	Ala	Gly	Val	Val	Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala
		35					40					45			

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser  
 50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser  
 65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp  
 85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile  
 100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu  
 115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr  
 130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro  
 145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val  
 165 170 175

Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val  
 180 185 190

Ala Met Val Arg Ala Phe Ser Glu Ser Asp  
 195 200

&lt;210&gt; 527

&lt;211&gt; 944

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(921)

&lt;223&gt; RXA01381

&lt;400&gt; 527

tcc gca ggc gtt gga acc atc acg gtc atc gat gac gac acc gtc gac 48  
 Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp  
 1 5 10 15

att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt 96  
 Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly  
 20 25 30

cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca 144  
 Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro  
 35 40 45

gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc 192  
 Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala  
 50 55 60

tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct 240  
 Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser

65	70	75	80	
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act	288			
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr				
85	90	95		
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc	336			
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu				
100	105	110		
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc	384			
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe				
115	120	125		
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt	432			
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly				
130	135	140		
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac	480			
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His				
145	150	155		
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc	528			
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile				
165	170	175		
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc	576			
Leu Ser Tyr Asp Ala Phe Pro Ala Thr Arg Ser Phe Arg Val Ser				
180	185	190		
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag	624			
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu				
195	200	205		
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc	672			
Ala Ala Arg Thr Asp Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly				
210	215	220		
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa	720			
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys				
225	230	235		
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc	768			
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile				
245	250	255		
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac	816			
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp				
260	265	270		
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac	864			
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp				
275	280	285		
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc	912			
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val				
290	295	300		
aac gcg ctg tagctgtcaa tttaagaggc cag	944			
Asn Ala Leu				
305				



&lt;210&gt; 528

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 528

Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp  
 1 5 10 15

Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly  
 20 25 30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro  
 35 40 45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala  
 50 55 60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser  
 65 70 75 80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr  
 85 90 95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu  
 100 105 110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe  
 115 120 125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly  
 130 135 140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His  
 145 150 155 160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile  
 165 170 175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser  
 180 185 190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu  
 195 200 205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly  
 210 215 220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys  
 225 230 235 240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile  
 245 250 255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp  
 260 265 270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp  
 275 280 285

Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val  
 290 295 300

Asn Ala Leu  
 305

<210> 529  
 <211> 259  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(259)  
 <223> RXA01360

<400> 529  
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gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115  
 Met Leu His Ile Ala  
 1 5

gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163  
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr  
 10 15 20

tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211  
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu  
 25 30 35

acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259  
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu  
 40 45 50

<210> 530  
 <211> 53  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 530  
 Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly  
 1 5 10 15

Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala  
 20 25 30

Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr  
 35 40 45

Thr Ser Ser Gly Glu  
 50

<210> 531  
 <211> 629  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(606)

&lt;223&gt; RXA01361

&lt;400&gt; 531

gcc gac gct gtg atc tct att gat ggc cac gat ccg tgt ttg acc gtg	48
Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val	
1 5 10 15	
acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg	96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu	
20 25 30	
gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg	144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala	
35 40 45	
aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc	192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg	
50 55 60	
gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt	240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe	
65 70 75 80	
gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc	288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu	
85 90 95	
gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc	336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly	
100 105 110	
gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att	384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile	
115 120 125	
gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc	432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr	
130 135 140	
ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg	480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala	
145 150 155 160	
tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca	528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala	
165 170 175	
cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt	576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu	
180 185 190	
gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga	626
Asp Val Cys Asp Pro Phe Arg His Gln Ile	
195 200	
tta	629

<210> 532  
 <211> 202  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 532  
 Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val  
 1 5 10 15  
 Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu  
 20 25 30  
 Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala  
 35 40 45  
 Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg  
 50 55 60  
 Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe  
 65 70 75 80  
 Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu  
 85 90 95  
 Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly  
 100 105 110  
 Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile  
 115 120 125  
 Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr  
 130 135 140  
 Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala  
 145 150 155 160  
 Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala  
 165 170 175  
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu  
 180 185 190  
 Asp Val Cys Asp Pro Phe Arg His Gln Ile  
 195 200

<210> 533  
 <211> 927  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(904)  
 <223> RXA01208

<400> 533  
 tactaggcac ggggtgccaa ccggatggaa aaattccgga ggctgagaaa acaccggttg 60  
 aacctgctct agctcgctact agcgaaggga tggccttaac gtg gct aac tcg ttt 115

																Val 1	Ala	Asn	Ser	Phe 5	
ttg	gat	tct	tta	act	ctt	gtt	cga	caa	aac	act	ccc	ctt	gtt	cag	tgt						163
Leu	Asp	Ser	Leu	Thr	Leu	Val	Arg	Gln	Asn	Thr	Pro	Leu	Val	Gln	Cys						
				10					15					20							
ttg	acc	aac	tct	gtg	gtc	atg	caa	ttc	acg	gcc	aat	gtg	ttg	ctt	gcc						211
Leu	Thr	Asn	Ser	Val	Val	Met	Gln	Phe	Thr	Ala	Asn	Val	Leu	Leu	Ala						
				25					30					35							
gcg	ggt	gcg	acc	cct	gcg	atg	gtg	gat	act	cca	gct	gaa	tcg	gca	gaa						259
Ala	Gly	Ala	Thr	Pro	Ala	Met	Val	Asp	Thr	Pro	Ala	Glu	Ser	Ala	Glu						
				40					45					50							
ttc	gcc	gct	gtg	gcc	aat	gga	gtg	ctc	atc	aat	gcg	gga	act	cct	tct						307
Phe	Ala	Ala	Val	Ala	Asn	Gly	Val	Leu	Ile	Asn	Ala	Gly	Thr	Pro	Ser						
				55					60					65							
gcg	gag	caa	tac	caa	ggc	atg	acc	aag	gcc	att	gag	ggt	gca	cga	aaa						355
Ala	Glu	Gln	Tyr	Gln	Gly	Met	Thr	Lys	Ala	Ile	Glu	Gly	Ala	Arg	Lys						
				70					75					80							
gct	ggc	aca	cca	tgg	gtg	tta	gac	cca	gtt	gct	gtg	ggt	ggg	ttg	tcg						403
Ala	Gly	Thr	Pro	Trp	Val	Leu	Asp	Pro	Val	Ala	Val	Gly	Gly	Leu	Ser						
				90					95					100							
gag	agg	acc	aag	tat	gcg	gag	gga	atc	gtc	gat	aag	cag	cct	gcc	gca						451
Glu	Arg	Thr	Lys	Tyr	Ala	Glu	Gly	Ile	Val	Asp	Lys	Gln	Pro	Ala	Ala						
				105					110					115							
att	cgt	gga	aac	gcc	tca	gag	gtc	gtg	gcg	ctt	gcg	ggg	ctc	ggt	gcc						499
Ile	Arg	Gly	Asn	Ala	Ser	Glu	Val	Val	Ala	Leu	Ala	Gly	Leu	Gly	Ala						
				120					125					130							
ggt	ggg	cgc	ggc	gta	gac	gcg	acc	gat	tcc	gtg	gaa	gtg	gcg	ttg	gag						547
Gly	Gly	Arg	Gly	Val	Asp	Ala	Thr	Asp	Ser	Val	Glu	Val	Ala	Leu	Glu						
				135					140					145							
gcg	gcg	caa	ttg	ttg	gcc	aag	cgc	act	ggt	ggc	gtc	gtg	gct	gtc	tct						595
Ala	Ala	Gln	Leu	Leu	Ala	Lys	Arg	Thr	Gly	Gly	Val	Val	Ala	Val	Ser						
				150					155					160							
ggt	gcg	gag	gac	ttg	att	gtg	tct	gcg	gat	cgg	gtg	acg	tgg	ttg	cgt						643
Gly	Ala	Glu	Asp	Leu	Ile	Val	Ser	Ala	Asp	Arg	Val	Thr	Trp	Leu	Arg						
				170					175					180							
tcg	ggg	gat	ccg	atg	ttg	cag	ctg	gtg	att	ggc	act	gga	tgc	tct	ttg						691
Ser	Gly	Asp	Pro	Met	Leu	Gln	Leu	Val	Ile	Gly	Thr	Gly	Cys	Ser	Leu						
				185					190					195							
ggc	gcg	ctg	aca	gct	gca	tat	cta	ggc	gcc	acg	gtt	gac	tca	gat	att						739
Gly	Ala	Leu	Thr	Ala	Ala	Tyr	Leu	Gly	Ala	Thr	Val	Asp	Ser	Asp	Ile						
				200					205					210							
tcc	gcg	cac	gat	gct	gtg	ttg	gct	gcg	cat	gcc	cat	gtg	ggt	gct	gct						787
Ser	Ala	His	Asp	Ala	Val	Leu	Ala	Ala	His	Ala	His	Val	Gly	Ala	Ala						
				215					220					225							
ggc	cag	att	gca	gca	cag	aag	gca	tcg	gcg	cca	ggc	agc	ttt	gcg	gtg						835
Gly	Gln	Ile	Ala	Ala	Gln	Lys	Ala	Ser	Ala	Pro	Gly	Ser	Phe	Ala	Val						

230                      235                      240                      245  
 gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg      883  
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser  
                                  250                      255                      260  
  
 ttg gtt gat gtg cga gag gcc tgaaaagtac gtgactgatt ttt      927  
 Leu Val Asp Val Arg Glu Ala  
                                  265  
  
 <210> 534  
 <211> 268  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
  
 <400> 534  
 Val Ala Asn Ser Phe Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr  
   1                                    5                                    10                                    15  
 Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala  
                                  20                                    25                                    30  
 Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro  
                                  35                                    40                                    45  
 Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn  
                                  50                                    55                                    60  
 Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile  
                                  65                                    70                                    75                                    80  
 Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala  
    85                                    90                                    95  
 Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp  
    100                                    105                                    110  
 Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu  
    115                                    120                                    125  
 Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val  
    130                                    135                                    140  
 Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly  
    145                                    150                                    155                                    160  
 Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg  
    165                                    170                                    175  
 Val Thr Trp Leu Arg Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly  
    180                                    185                                    190  
 Thr Gly Cys Ser Leu Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr  
    195                                    200                                    205  
 Val Asp Ser Asp Ile Ser Ala His Asp Ala Val Leu Ala Ala His Ala  
    210                                    215                                    220  
 His Val Gly Ala Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro  
    225                                    230                                    235                                    240

Gly Ser Phe Ala Val Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala  
245 250 255

Gln Ala Val Ala Ser Leu Val Asp Val Arg Glu Ala  
260 265

**<210> 535**

<211> 1023

<212> DNA

<213> Corynebacterium glutamicum

**<220>**

**<221> CDS**

<222> (101) . . (1000)

<223> RXA00838

<400> 535

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tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115  
Met Lys Ile Ala Ile  
1 5

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163  
Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu  
10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211  
Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala  
25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259  
Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr  
40 45 50

gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat 307  
Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp  
55 60 65

gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct 355  
Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala  
70 75 80 85

gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag 403  
Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln  
90 95 100

aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451  
Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp  
105 110 115

cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499  
 Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro  
 120 125 130

gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547  
Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp  
135 140 145

tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595  
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly  
 150 155 160 165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643  
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys  
 170 175 180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691  
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys  
 185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739  
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu  
 200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787  
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro  
 215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835  
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu  
 230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883  
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser  
 250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931  
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val  
 265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979  
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu  
 280 285 290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg  
 1023  
 Lys Glu Glu Glu Asn Ser Leu  
 295 300

<210> 536  
 <211> 300  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 536  
 Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly  
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 Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly  
 20 25 30  
 Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala  
 35 40 45  
 Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu  
 50 55 60  
 Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg



65	70	75	80
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr	275	280	285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu	290	295	300

&lt;210&gt; 537

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(670)

&lt;223&gt; RXA02400

&lt;400&gt; 537

aggtgcccc aacgttgcc tttgactgca aattttccga aagaatccat aaactacttc 60

tttaagtcgc cagattaaag tctgcaatga aaggacatac atg tct att tcc cgc 115

Met Ser Ile Ser Arg

1 5

acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt	163
Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val	
10 15 20	
gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat	211
Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn	
25 30 35	
gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca	259
Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser	
40 45 50	
acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta	307
Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val	
55 60 65	
gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc	355
Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr	
70 75 80 85	
ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc	403
Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile	
90 95 100	
tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc	451
Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly	
105 110 115	
gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc	499
Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro	
120 125 130	
ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt	547
Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu	
135 140 145	
gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt	595
Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys	
150 155 160 165	
gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct	643
Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala	
170 175 180	
gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac	690
Glu Val Pro Val Thr Phe Ala Ala Ala	
185 190	
tca	693

&lt;210&gt; 538

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 538

Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu
1 5 10 15

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<210> 539
<211> 1528
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1528)
<223> RXN01209
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<400> 539
cagattgcag cacagaaggc atcggcgcca ggcagctttg cgggtggcgtt tattgatgcg 60

ctttatgacg tggatgcccc ggctgtggcc tcgttggttg atg tgc gag agg cct 115
                                         Met Cys Glu Arg Pro
                                         1                               5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
                        10                               15                               20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
                        25                               30                               35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val

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40	45	50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala 55 60 65			307
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu 70 75 80 85			355
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa Leu Gly Leu His Leu His Ile Gly Gln Asp Thr Pro Tyr Thr Gln 90 95 100			403
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu 105 110 115			451
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly 120 125 130			499
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala 135 140 145			547
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu 150 155 160 165			595
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly 170 175 180			643
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp 185 190 195			691
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala 200 205 210			739
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu 215 220 225			787
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn 230 235 240 245			835
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr 250 255 260			883
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly 265 270 275			931
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His 280 285 290			979

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123  
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459  
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465

gcc gcc ggc gaa agc gtg gaa  
 1528  
 Ala Ala Gly Glu Ser Val Glu  
 470 475

&lt;210&gt; 540

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 540

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Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu
  1              5              10              15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile
      20              25              30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
      35              40              45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
      50              55              60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
      65              70              75              80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
      85              90              95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
      100              105              110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
      115              120              125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
      130              135              140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
      145              150              155              160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
      165              170              175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
      180              185              190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
      195              200              205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
      210              215              220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
      225              230              235              240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
      245              250              255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
      260              265              270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
      275              280              285

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Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg  
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser  
 450 455 460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu  
 465 470 475

&lt;210&gt; 541

&lt;211&gt; 1528

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1528)

&lt;223&gt; FRXA01209

&lt;400&gt; 541

cagattgcag cacagaaggc atcggcgcca ggcagctttg cgggtggcggtt tattgatgcg 60

ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115  
 Met Cys Glu Arg Pro  
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163  
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val  
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211  
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile  
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
40 45 50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
55 60 65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	



ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979  
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His  
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag  
 1027  
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln  
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc  
 1075  
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly  
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt  
 1123  
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly  
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc  
 1171  
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr  
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc  
 1219  
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg  
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc  
 1267  
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala  
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct  
 1315  
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala  
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag  
 1363  
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys  
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc  
 1411  
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro  
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac  
 1459  
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn  
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc  
 1507  
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile  
 455 460 465

gcc gcc ggc gaa agc gtg gaa  
 1528

Ala Ala Gly Glu Ser Val Glu  
470 475

<210> 542

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 542

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu  
1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile  
20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp  
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys  
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu  
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp  
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu  
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln  
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro  
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val  
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala  
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala  
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala  
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro  
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln  
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala  
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser  
260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val  
 275 280 285

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr  
 290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp  
 305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val  
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro  
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu  
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn  
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met  
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr  
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn  
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg  
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser  
 450 455 460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu  
 465 470 475

&lt;210&gt; 543

&lt;211&gt; 723

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(700)

&lt;223&gt; RXN01413

&lt;400&gt; 543

tttgcctat tggaagaagt aaattccaca ccttcacttt ccaatacttc ttttggtgag 60

cgggtttcct cagcgtttta ccatctgaaa ccatctgaga ttg acc cat ctg ttc 115  
 Leu Thr His Leu Phe  
 1 5

tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163  
 Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr  
 10 15 20

```

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211
Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
      25                      30                      35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259
Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
      40                      45                      50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307
Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Pro Gln Ala Thr
      55                      60                      65

gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355
Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
      70                      75                      80                      85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403
Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
      90                      95                      100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451
Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
      105                      110                      115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc 499
Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
      120                      125                      130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547
Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
      135                      140                      145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595
Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
      150                      155                      160                      165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643
Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
      170                      175                      180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691
Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
      185                      190                      195

gac aac aag tagagtttta aaataccgat caa 723
Asp Asn Lys
      200

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&lt;210&gt; 544

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 544

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Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val
  1                      5                      10                      15
Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu
      20                      25                      30

```

Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg  
           35                                  40                                  45  
 Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu  
           50                                  55                                  60  
 Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr  
           65                                  70                                  75                                  80  
 Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala  
                                   85                                  90                                  95  
 Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly  
                                   100                                  105                                  110  
 Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly  
           115                                  120                                  125  
 Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val  
           130                                  135                                  140  
 Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala  
           145                                  150                                  155                                  160  
 Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val  
                                   165                                  170                                  175  
 Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser  
           180                                  185                                  190  
 Val Trp Leu Ala Glu Asp Asn Lys  
           195                                  200

&lt;210&gt; 545

&lt;211&gt; 795

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(772);

&lt;223&gt; RXN01617

&lt;400&gt; 545

tcagaagcta ccggcggcgc cggcatccag gttgatttga agaccttcca gcatttaaga 60  
 tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115  
   Leu Ile Leu Lys Thr  
   1                                  5  
 act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163  
 Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn  
                                   10                                  15                                  20  
 cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211  
 Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile  
                                   25                                  30                                  35  
 ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259  
 Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu

40	45	50	
gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc			307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys			
55	60	65	
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc			355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg			
70	75	80	85
gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag			403
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu			
	90	95	100
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu			
	105	110	115
aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt			499
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val			
	120	125	130
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt			547
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
	135	140	145
ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac			595
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
150	155	160	165
gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca			643
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
	170	175	180
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
	185	190	195
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
	200	205	210
ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc			792
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
215	220		
cct			795
<210> 546			
<211> 224			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 546			
Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala			
1	5	10	15
Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu			
	20	25	30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr  
                   35                                  40                                  45  
 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp  
                   50                                  55                                  60  
 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr  
                   65                                  70                                  75                                  80  
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr  
                                   85                                  90                                  95  
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu  
                                  100                                 105                                 110  
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly  
                   115                                 120                                 125  
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn  
                   130                                 135                                 140  
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu  
                   145                                 150                                 155                                 160  
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala  
                                  165                                 170                                 175  
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala  
                                  180                                 185                                 190  
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val  
                   195                                 200                                 205  
 Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys  
                   210                                 215                                 220

&lt;210&gt; 547

&lt;211&gt; 638

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (615)

&lt;223&gt; FRXA01617

&lt;400&gt; 547

gct aat cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg 48  
 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val  
           1                                  5                                  10                                  15  
 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96  
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr  
                   20                                  25                                  30  
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144  
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu

35	40	45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc			192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			
50	55	60	
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac			240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn			
65	70	75	80
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac			288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp			
85	90	95	
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac			336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
100	105	110	
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac			384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			
115	120	125	
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc			432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile			
130	135	140	
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc			480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile			
145	150	155	160
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc			528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr			
165	170	175	
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac			576
Ala Lys Arg Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn			
180	185	190	
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt			625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
195	200	205	
aaacaagctc cct			638

&lt;210&gt; 548

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 548

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
1 5 10 15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
20 25 30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
35 40 45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala
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50	55	60
Leu Arg Ala Lys Val 65	Leu Pro Gln Ala Thr 70	Val Val Thr Pro Asn Asn 75 80
Phe Glu Ala Thr Thr 85	Leu Ser Gly Leu Asp 90	Lys Leu Glu Thr Ile Asp 95
Asp Leu Lys Glu Ala 100	Ala Arg Leu Ile His 105	Glu Gln Gly Pro Gln Tyr 110
Val Val Val Lys Gly 115	Gly Ile Asp Phe Pro 120	Gly Asp Asn Ala Val Asp 125
Val Leu Phe Asp Gly 130	Thr Asp Tyr His Val 135	Phe Ser Glu Pro Lys Ile 140
Gly Asp Glu Arg Val 145	Ser Gly Ala Gly Cys 150 155	Thr Phe Ala Ala Val Ile 160
Thr Ala Glu Leu Ala 165	Lys Gly Asn Ser Ala 170	Val Asp Ala Val Thr Thr 175
Ala Lys Arg Val Val 180	Thr Arg Ala Val Lys 185	Asp Ala Val Ala Ser Asn 190
Ala Pro Phe Thr Ser 195	Val Trp Leu Ala Glu 200	Asp Asn Lys 205

&lt;210&gt; 549

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(892)

&lt;223&gt; RXS01807

&lt;400&gt; 549

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gctcaccgag ctggacacca agctccgcg agtgcaggaa gaacacggcg agctggaaat 60
gcagtggctg gaactcggcg aggaaatcga gggctagttc atg ccg tcg gca ggc 115
                                     Met Pro Ser Ala Gly
                                     1 5

gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163
Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg
                                     10 15 20

gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211
Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly
                                     25 30 35

ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259
Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val
                                     40 45 50

gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307
Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser

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55	60	65	
cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac			355
His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp			
70	75	80	85
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc			403
Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly			
	90	95	100
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag			451
Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln			
	105	110	115
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc			499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile			
	120	125	130
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc			547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr			
	135	140	145
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat			595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn			
	150	155	160
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg			643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu			
	170	175	180
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act			691
Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr			
	185	190	195
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa			739
Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu			
	200	205	210
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc			787
Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val			
	215	220	225
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc			835
Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile			
	230	235	240
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc			883
Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr			
	250	255	260
aaa gcg ctt taggtttcgt ccgtctctga cag			915
Lys Ala Leu			

&lt;210&gt; 550

&lt;211&gt; 264

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 550

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Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu
 1           5           10           15
Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
           20           25           30
Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
           35           40           45
Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50           55           60
Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65           70           75           80
Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
           85           90           95
Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
           100          105          110
Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
           115          120          125
Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
           130          135          140
Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
           145          150          155          160
Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
           165          170          175
Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
           180          185          190
Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
           195          200          205
Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
           210          215          220
Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
           225          230          235          240
Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
           245          250          255
Ala Gly Leu Gln Thr Lys Ala Leu
           260

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&lt;210&gt; 551

&lt;211&gt; 622

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(622)

&lt;223&gt; RXC01021

&lt;400&gt; 551

cgagaggctt ttttggctct aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115  
 Met Ser Ser Ser Glu  
 1 5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163  
 Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu  
 10 15 20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211  
 Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala  
 25 30 35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259  
 Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala  
 40 45 50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307  
 Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val  
 55 60 65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355  
 Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met  
 70 75 80 85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403  
 Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val  
 90 95 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451  
 Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg  
 105 110 115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499  
 Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln  
 120 125 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547  
 Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu  
 135 140 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595  
 Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu  
 150 155 160 165

ggc act gtt gtc act gtg ttg cgt tct 622  
 Gly Thr Val Val Thr Val Leu Arg Ser  
 170

&lt;210&gt; 552

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 552

Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro  
 1 5 10 15

<400> 553																	
tgccgacgct	ggcgtggatg	ccttcgttgc	aggttccgct	gtgtacggcg	ctgaggatcc												60
caacaaggcg atccaggagt tgcgagcact cgcgcagtaa atg gat gtt gcg cac																	115
Met Asp Val Ala His																	
1 5																	
gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc																	163
Ala	Leu	Asp	Leu	Ala	His	His	Val	Ser	Asp	Gln	Val	Arg	Gly	Thr	Thr		
10 15 20																	
agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag																	211
Ser	Pro	Asn	Pro	Pro	Val	Gly	Ala	Val	Ile	Leu	Asp	Ala	Asp	Gly	Glu		
25 30 35																	
gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa																	259
Val	Val	Gly	Val	Gly	Ala	Thr	Ala	Pro	Pro	Gly	Gly	Pro	His	Ala	Glu		
40 45 50																	

gtg	gtg	gcg	ctt	gca	gct	gcc	gga	gtg	cgt	gcc	aac	ggg	ggc	acg	gcg	307
Val	Val	Ala	Leu	Ala	Ala	Ala	Gly	Val	Arg	Ala	Asn	Gly	Gly	Thr	Ala	
55						60					65					
gtg	gtc	acc	ctc	gag	ccg	tgc	aac	cat	tac	ggc	cgc	acg	ggg	cca	tgt	355
Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly	Arg	Thr	Gly	Pro	Cys	
70					75					80					85	
tcc	aag	gcg	ctt	ctc	gac	gcc	ggg	atc	gca	cac	gtg	ttt	tac	gcc	aat	403
Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His	Val	Phe	Tyr	Ala	Asn	
				90					95					100		
gcg	gat	ccc	ttc	ccg	tca	gcc	gct	ggg	ggc	ggg	gcc	ttt	ttg	gcg	gag	451
Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	Gly	Ala	Phe	Leu	Ala	Glu	
			105					110					115			
gcg	ggc	gtc	gat	acg	cat	ttt	tta	gat	gag	cgg	atc	agg	gca	ctg	gag	499
Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	Arg	Ile	Arg	Ala	Leu	Glu	
		120					125					130				
ccc	tgg	ctg	gtt	gcg	acg	cgt	ctg	ggc	agg	ccc	cat	gtc	acg	ttg	aag	547
Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro	His	Val	Thr	Leu	Lys	
	135					140					145					
ttt	gcg	tcc	acc	gtg	gac	ggg	ttt	gct	ggg	gcc	acc	gat	ggc	acc	agc	595
Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala	Thr	Asp	Gly	Thr	Ser	
150					155					160					165	
cag	tgg	att	acc	ggg	ccg	gat	gcg	cgg	gcg	ttt	gtg	cac	gaa	gat	cga	643
Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe	Val	His	Glu	Asp	Arg	
				170					175					180		
agt	aaa	aga	gat	gcg	atc	atc	gtg	ggg	acc	ggg	act	gcg	ttg	act	gat	691
Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly	Thr	Ala	Leu	Thr	Asp	
			185					190					195			
aat	ccc	tcc	ttg	acg	gcg	cgg	acc	gat	acg	ggg	ctt	tat	gaa	aat	caa	739
Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly	Leu	Tyr	Glu	Asn	Gln	
		200					205					210				
ccc	agg	cgc	gtt	gtt	att	ggc	tcc	cgc	gag	gtt	cca	gca	gat	tcc	aac	787
Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val	Pro	Ala	Asp	Ser	Asn	
	215					220					225					
ttg	gct	cgc	ttg	gga	tat	gag	cag	tac	gcg	gga	ata	cca	gag	gct	tta	835
Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly	Ile	Pro	Glu	Ala	Leu	
230					235					240					245	
tca	gcg	ctg	tgg	gat	aaa	ggg	tgc	cga	gac	att	tta	atc	gaa	ggg	ggc	883
Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile	Leu	Ile	Glu	Gly	Gly	
				250					255					260		
cca	acg	tta	gct	ggg	gca	gcg	ctg	cgc	tta	ggc	att	gtt	gat	cag	gtg	931
Pro	Thr	Leu	Ala	Gly	Ala	Ala	Leu	Arg	Leu	Gly	Ile	Val	Asp	Gln	Val	
			265					270					275			
cag	gcc	tat	gtt	gcc	ccc	gct	ttg	ttg	ggc	gct	gga	cga	tca	gtg	att	979
Gln	Ala	Tyr	Val	Ala	Pro	Ala	Leu	Leu	Gly	Ala	Gly	Arg	Ser	Val	Ile	
		280					285					290				

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc  
1027

Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr  
295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga  
1075

Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg  
310 315 320 325

aag gaa cac taaatgttca caggtattgt cga  
1107

Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln  
1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu  
20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly  
35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala  
50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly  
65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His  
85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly  
100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg  
115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro  
130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala  
145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe  
165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly  
180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly  
195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val  
 210 215 220  
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly  
 225 230 235 240  
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile  
 245 250 255  
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly  
 260 265 270  
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala  
 275 280 285  
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile  
 290 295 300  
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu  
 305 310 315 320  
 Ile Glu Met Met Arg Lys Glu His  
 325

<210> 555  
 <211> 1107  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1084)  
 <223> FRXA02246

<400> 555  
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 caacaaggcg atccaggagt tgcgagcact cgcgcagtaa atg gat gtt gcg cac 115  
 Met Asp Val Ala His  
 1 5  
 gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163  
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr  
 10 15 20  
 agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211  
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu  
 25 30 35  
 gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259  
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu  
 40 45 50  
 gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307  
 Val Val Ala Leu Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala  
 55 60 65  
 gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355  
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys  
 70 75 80 85



tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat	403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn	
90 95 100	
gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag	451
Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu	
105 110 115	
gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag	499
Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu	
120 125 130	
ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag	547
Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys	
135 140 145	
ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc	595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	
150 155 160 165	
cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga	643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg	
170 175 180	
agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat	691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp	
185 190 195	
aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa	739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln	
200 205 210	
ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn	
215 220 225	
ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu	
230 235 240 245	
tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly	
250 255 260	
cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg	931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val	
265 270 275	
cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att	979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	
280 285 290	
aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc	1027
Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr	
295 300 305	
acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga	1075
Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg	

310

315

320

325

aag gaa cac taaatgttca caggtattgt cga  
 1107  
 Lys Glu His

&lt;210&gt; 556

&lt;211&gt; 328

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 556

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln  
 1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu  
 20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly  
 35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala  
 50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly  
 65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His  
 85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly  
 100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg  
 115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro  
 130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala  
 145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe  
 165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly  
 180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly  
 195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val  
 210 215 220

Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly  
 225 230 235 240

Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile  
 245 250 255

[illegible]

<210> 557

<211> 756

<212> DNA

<213> *Corynebacterium glutamicum*

**<220>**

<221> CDS

<222> (101) .. (733)

<223> RXA02247

**<400> 557**

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              Met Phe Thr Gly Ile
              1           5

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gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163  
Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser  
10 15 20

atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211  
Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu  
25 30 35

ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt 259  
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe  
 40 45 50

ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307  
Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg  
55 60 65

agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355  
 Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg  
 70 75 80 85

gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403  
Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His  
90 95 100

gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451  
Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp  
105 110 115

gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499  
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val  
120 125 130

gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct 547  
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser  
135 140 145

ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc 595  
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg  
150 155 160 165

gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag 643  
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu  
170 175 180

gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691  
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val  
185 190 195

gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733  
Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp  
200 205 210

taggttagac aacgtgagtg aac 756

&lt;210&gt; 558

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 558

Met Phe Thr Gly Ile Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu  
1 5 10 15

His Leu Gly Asp Ser Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu  
20 25 30

Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu  
35 40 45

Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln  
50 55 60

Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys  
65 70 75 80

Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His  
85 90 95

Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr  
100 105 110

Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu  
115 120 125

Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser  
130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile  
 145 150 155 160  
 Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp  
 165 170 175  
 Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met  
 180 185 190  
 Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe  
 195 200 205  
 Thr Arg Asp  
 210

<210> 559  
 <211> 1389  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1366)  
 <223> RXN02248

<400> 559  
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 aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115  
 Val Ser Glu His Glu  
 1 5  
 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163  
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile  
 10 15 20  
 gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211  
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn  
 25 30 35  
 gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259  
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val  
 40 45 50  
 gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307  
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr  
 55 60 65  
 gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355  
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn  
 70 75 80 85  
 cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403  
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr  
 90 95 100  
 ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451  
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu  
 105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499  
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His  
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547  
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly  
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595  
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro  
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643  
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met  
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691  
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys  
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739  
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile  
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787  
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr  
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835  
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val  
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883  
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu  
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931  
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg  
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979  
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln  
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga  
 1027  
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg  
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa  
 1075  
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu  
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat  
 1123  
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp  
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg  
 1171

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val  
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt  
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu  
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct  
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala  
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg  
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met  
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa  
 1363

Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu  
 410 415 420

aac taaggagcac aacaatggct aaa  
 1389  
 Asn

<210> 560  
 <211> 422  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 560

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu  
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 20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala  
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile  
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro  
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr  
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala  
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe  
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val  
 130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala  
 145 150 155 160  
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu  
 165 170 175  
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp  
 180 185 190  
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg  
 195 200 205  
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro  
 210 215 220  
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp  
 225 230 235 240  
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly  
 245 250 255  
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp  
 260 265 270  
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser  
 275 280 285  
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg  
 290 295 300  
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr  
 305 310 315 320  
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu  
 325 330 335  
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu  
 340 345 350  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala  
 355 360 365  
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr  
 370 375 380  
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr  
 385 390 395 400  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu  
 405 410 415  
 Gln Glu His Pro Glu Asn  
 420

&lt;210&gt; 561

&lt;211&gt; 1389

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1366)

&lt;223&gt; FRXA02248

&lt;400&gt; 561

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gatgtgatcg ctaagtacgt cgaacgcatg atgacgcgcg gcgtggctgg aaacactccc 60

aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
Val Ser Glu His Glu
1 5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
10 15 20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
25 30 35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
40 45 50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
55 60 65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
70 75 80 85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
90 95 100

ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739

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Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile	
200 205 210	
ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg	787
Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr	
215 220 225	
ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt	835
Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val	
230 235 240 245	
gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg	883
Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu	
250 255 260	
gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg	931
Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg	
265 270 275	
cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag	979
Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln	
280 285 290	
gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga	
1027	
Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg	
295 300 305	
ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa	
1075	
Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu	
310 315 320 325	
ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat	
1123	
Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp	
330 335 340	
gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg	
1171	
Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val	
345 350 355	
cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt	
1219	
Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu	
360 365 370	
gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct	
1267	
Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala	
375 380 385	
gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg	
1315	
Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met	
390 395 400 405	
gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa	
1363	
Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu	

410

415

420

aac taaggagcac aacaatggct aaa  
1389  
Asn

&lt;210&gt; 562

&lt;211&gt; 422

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 562

Val	Ser	Glu	His	Glu	Gln	Ala	His	Ser	Gln	Leu	Asp	Ser	Val	Glu	Glu
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Ala	Ile	Ala	Asp	Ile	Ala	Ala	Gly	Lys	Ala	Val	Val	Val	Val	Asp	Asp
			20					25					30		
Glu	Asp	Arg	Glu	Asn	Glu	Gly	Asp	Ile	Ile	Phe	Ala	Ala	Glu	Leu	Ala
	35						40					45			
Thr	Pro	Glu	Leu	Val	Ala	Phe	Met	Val	Arg	Tyr	Ser	Ser	Gly	Tyr	Ile
	50					55					60				
Cys	Ala	Pro	Leu	Thr	Ala	Lys	Asp	Ala	Asp	Arg	Leu	Asp	Leu	Pro	Pro
65					70					75				80	
Met	Thr	Ala	His	Asn	Gln	Asp	Ala	Arg	Gly	Thr	Ala	Tyr	Thr	Val	Thr
				85					90					95	
Val	Asp	Ala	Asn	Thr	Gly	Thr	Thr	Gly	Ile	Ser	Ala	Thr	Asp	Arg	Ala
			100					105					110		
His	Thr	Leu	Arg	Leu	Leu	Ala	Asp	Pro	Glu	Ala	Asp	Arg	Thr	Asp	Phe
	115						120					125			
Thr	Arg	Pro	Gly	His	Val	Val	Pro	Leu	Arg	Ala	Arg	Glu	Gly	Gly	Val
	130					135					140				
Leu	Val	Arg	Ala	Gly	His	Thr	Glu	Ala	Ala	Val	Asp	Leu	Ala	Arg	Ala
145					150					155				160	
Ala	Gly	Leu	Arg	Pro	Ala	Gly	Val	Ile	Cys	Glu	Val	Val	Ser	Glu	Glu
				165					170					175	
Asp	Pro	Thr	Gly	Met	Ala	Arg	Val	Pro	Glu	Leu	Arg	Arg	Phe	Cys	Asp
		180						185					190		
Glu	His	Asp	Leu	Lys	Leu	Ile	Ser	Ile	Glu	Gln	Leu	Ile	Glu	Trp	Arg
	195						200					205			
Arg	Lys	Asn	Glu	Ile	Leu	Val	Glu	Arg	Gln	Val	Glu	Thr	Val	Leu	Pro
	210					215					220				
Thr	Asp	Phe	Gly	Thr	Phe	Lys	Ala	Val	Gly	Tyr	Arg	Ser	Ile	Ile	Asp
225					230					235				240	
Gly	Thr	Glu	Leu	Val	Ala	Ile	Val	Ala	Gly	Asp	Val	Ala	Ser	Asp	Gly
			245						250					255	

Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp  
 260 265 270  
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser  
 275 280 285  
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg  
 290 295 300  
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr  
 305 310 315 320  
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu  
 325 330 335  
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu  
 340 345 350  
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala  
 355 360 365  
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr  
 370 375 380  
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr  
 385 390 395 400  
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu  
 405 410 415  
 Gln Glu His Pro Glu Asn  
 420

<210> 563  
 <211> 600  
 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
 <221> CDS  
 <222> (101)..(577)  
 <223> RXN02249

<400> 563  
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 tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115  
 Met Ala Lys Glu Gly  
 1 5  
 ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163  
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val  
 10 15 20  
 gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211  
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His  
 25 30 35  
 gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259

Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg  
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307  
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg  
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355  
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr  
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403  
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg  
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451  
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr  
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499  
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val  
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547  
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu  
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597  
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly  
150 155

ttg 600

&lt;210&gt; 564

&lt;211&gt; 159

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 564

Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly  
1 5 10 15

Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp  
20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr  
35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val  
50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val  
65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr  
85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn  
100 105 110